

FIG. 1A

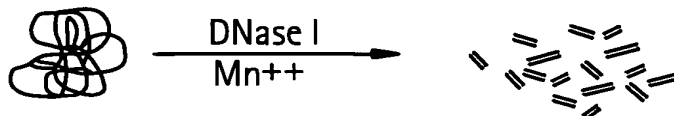


FIG. 1B

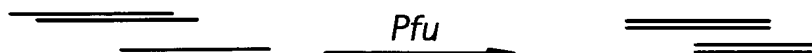


FIG. 1C

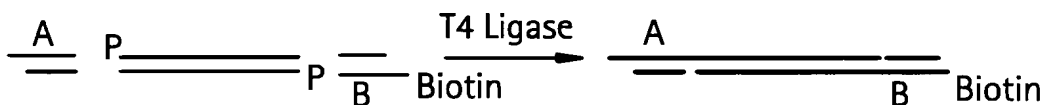


FIG. 1D

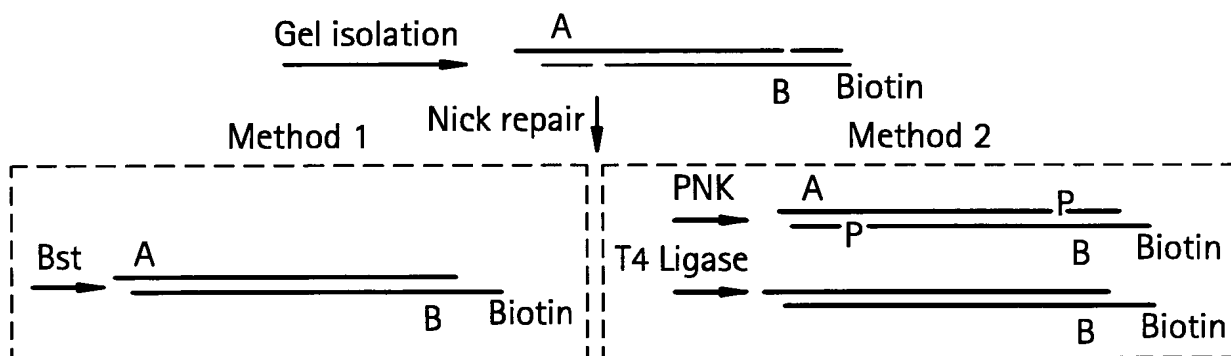


FIG. 1E

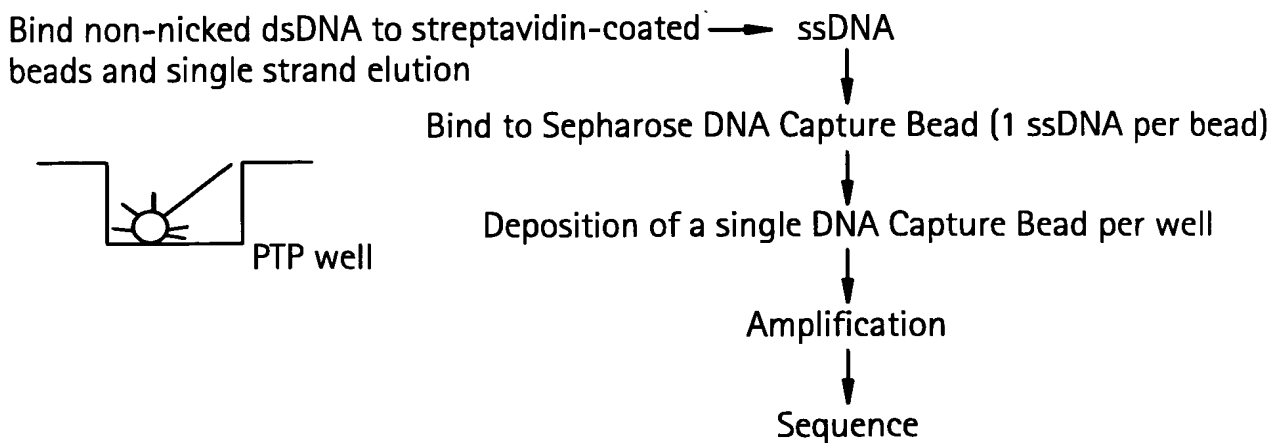


FIG. 1F

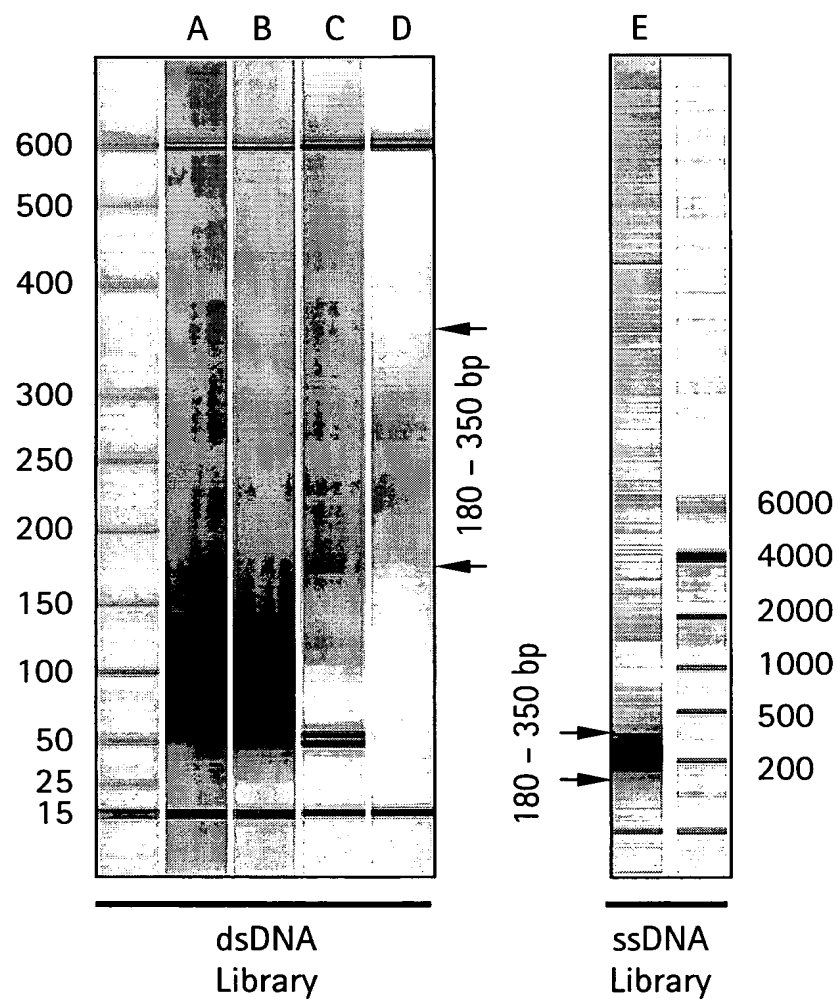


FIG. 1G

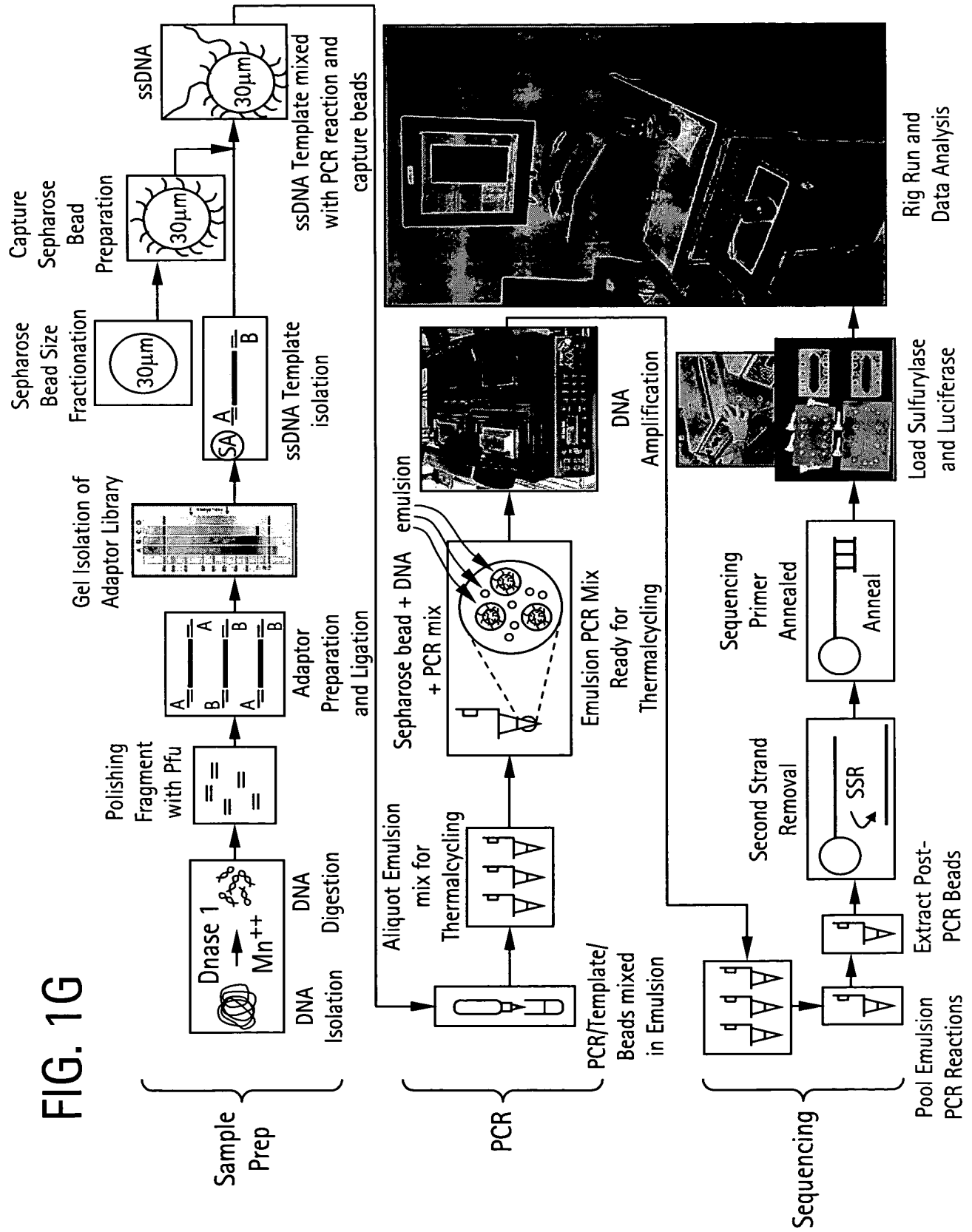


FIG. 2A

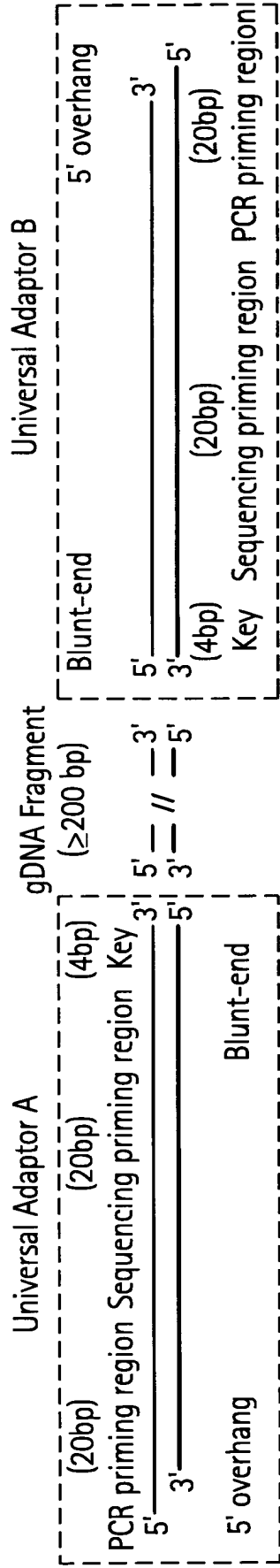


FIG. 2B



FIG. 2C

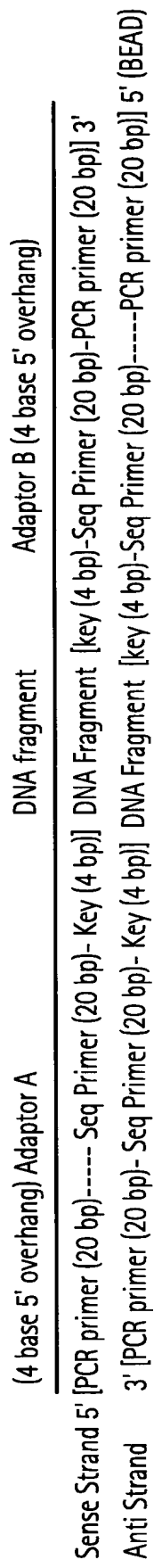


FIG. 3A

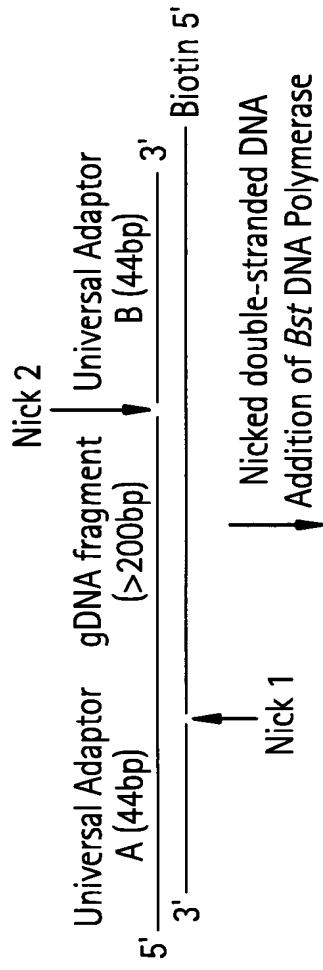


FIG. 3B

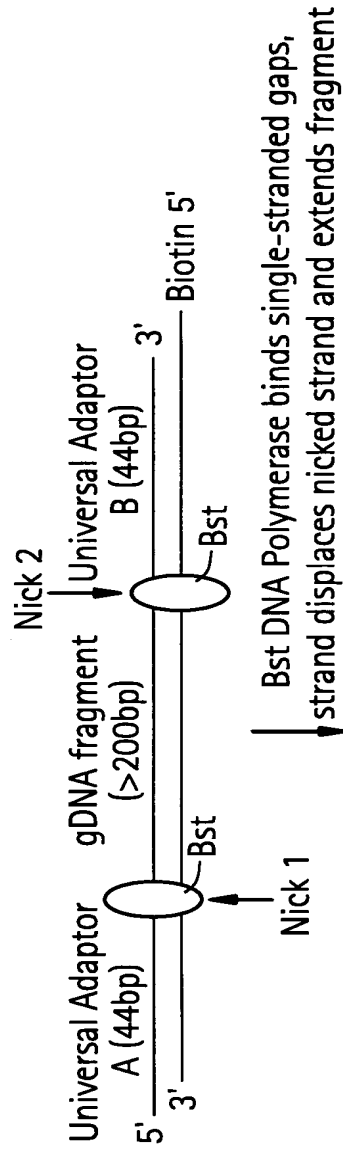


FIG. 3C

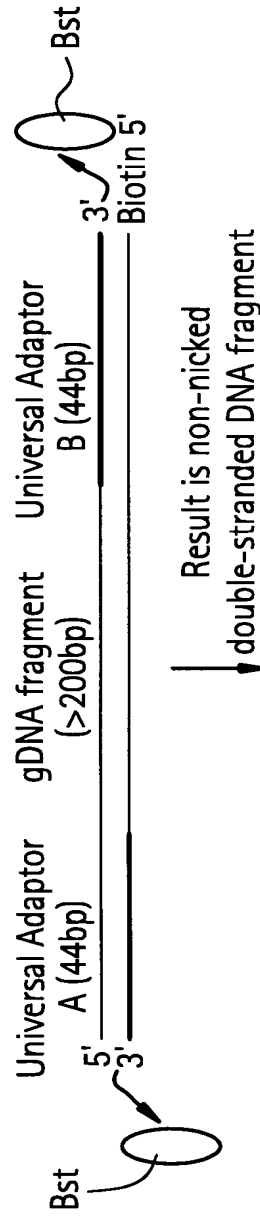


FIG. 3D

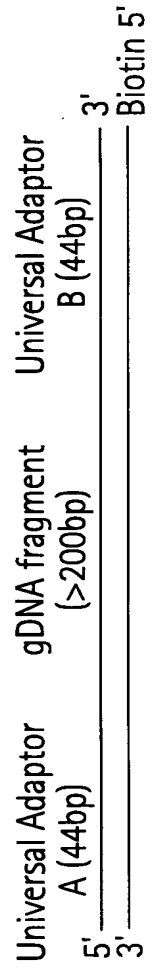


FIG. 4

Possible double-stranded Genomic DNA Library Species:

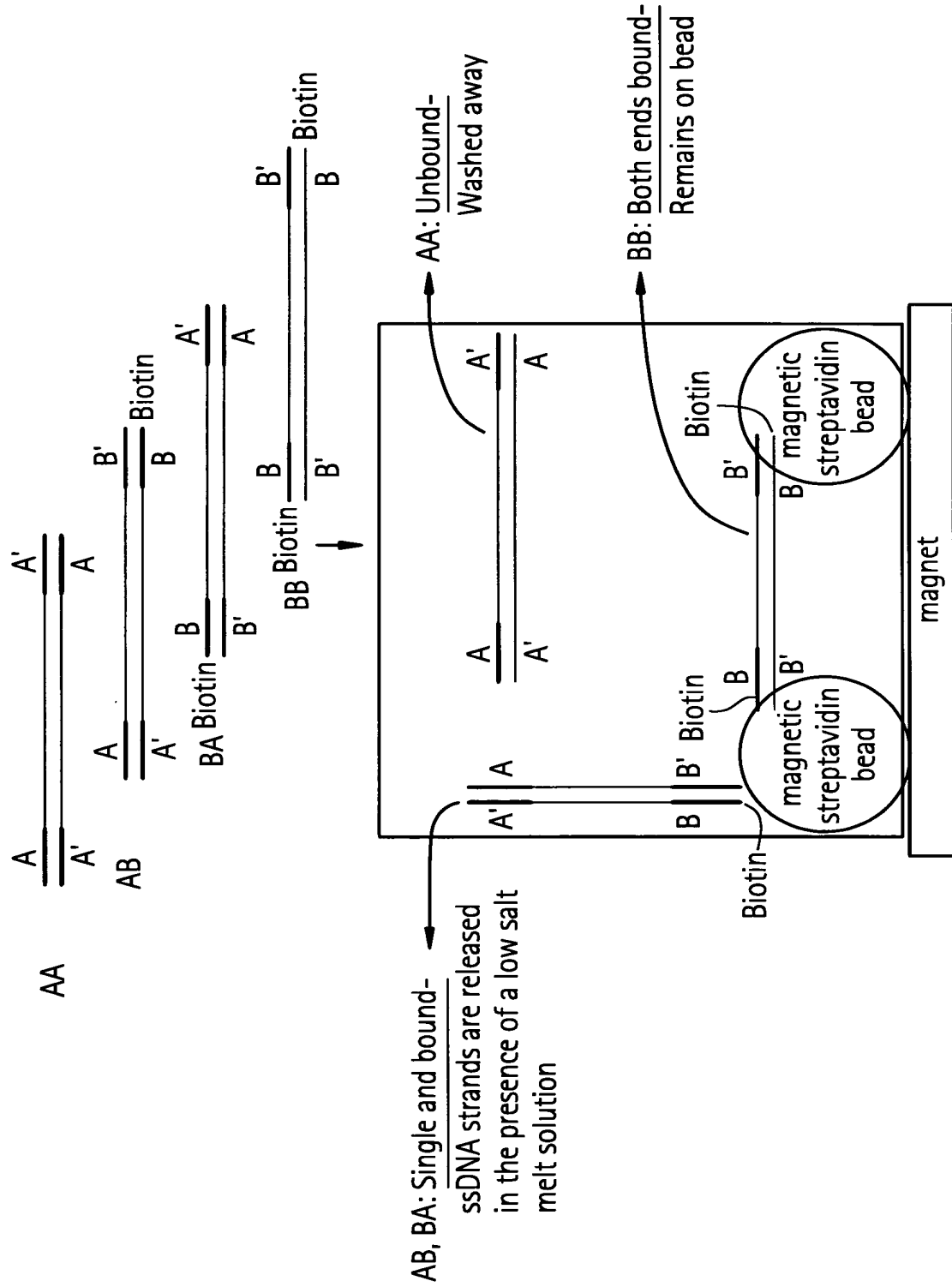


FIG. 5

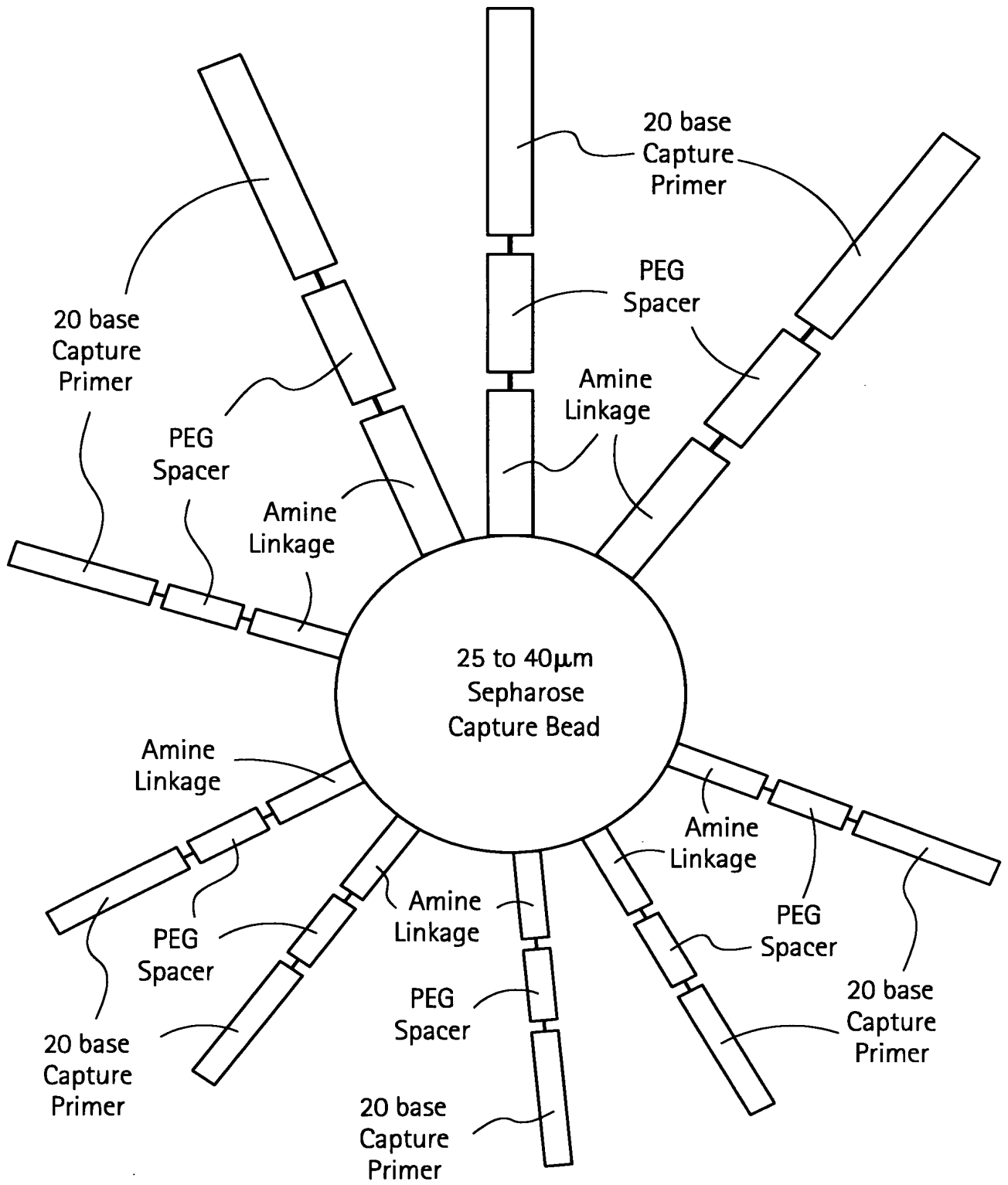


FIG. 6A

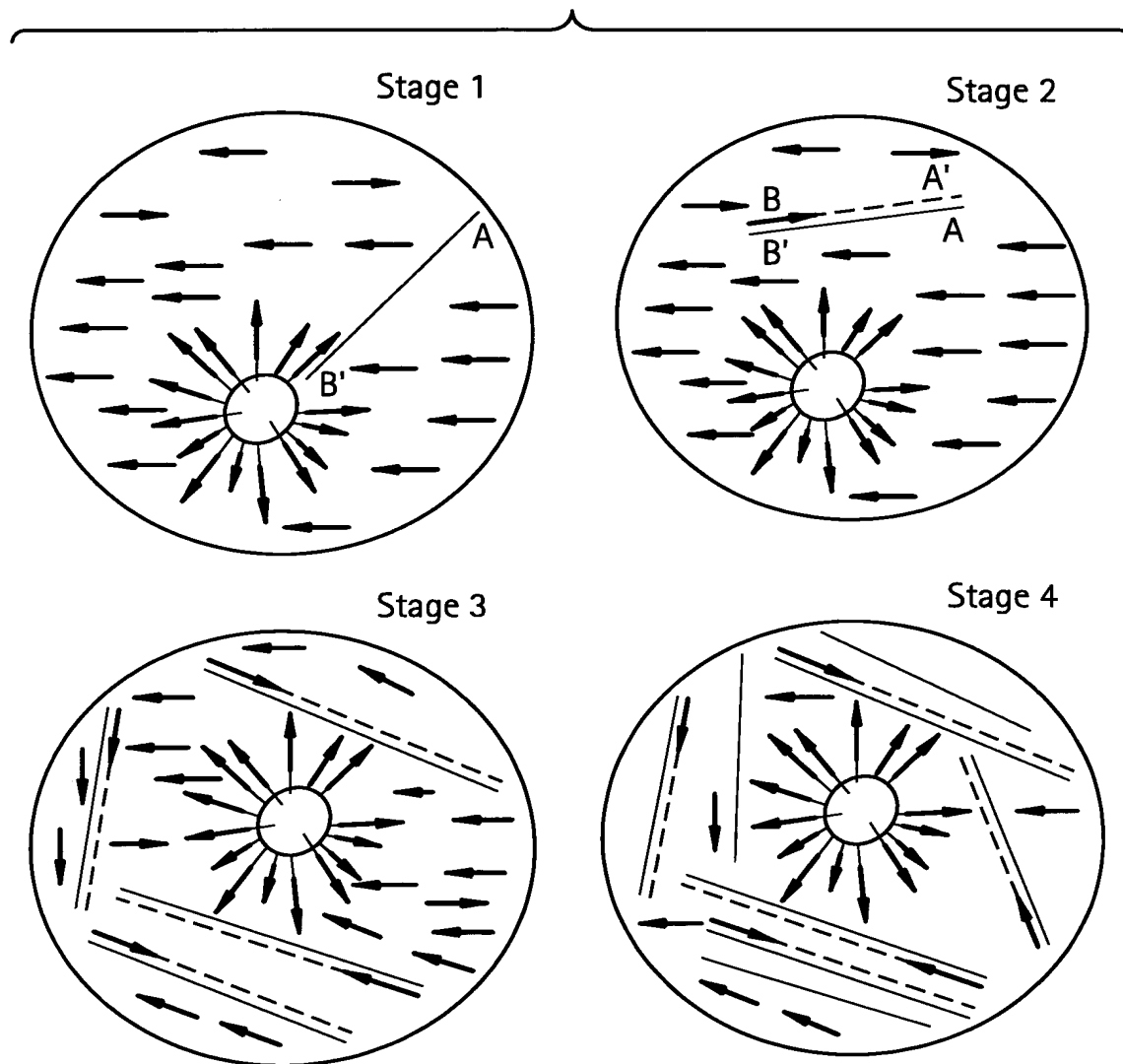


FIG. 6B

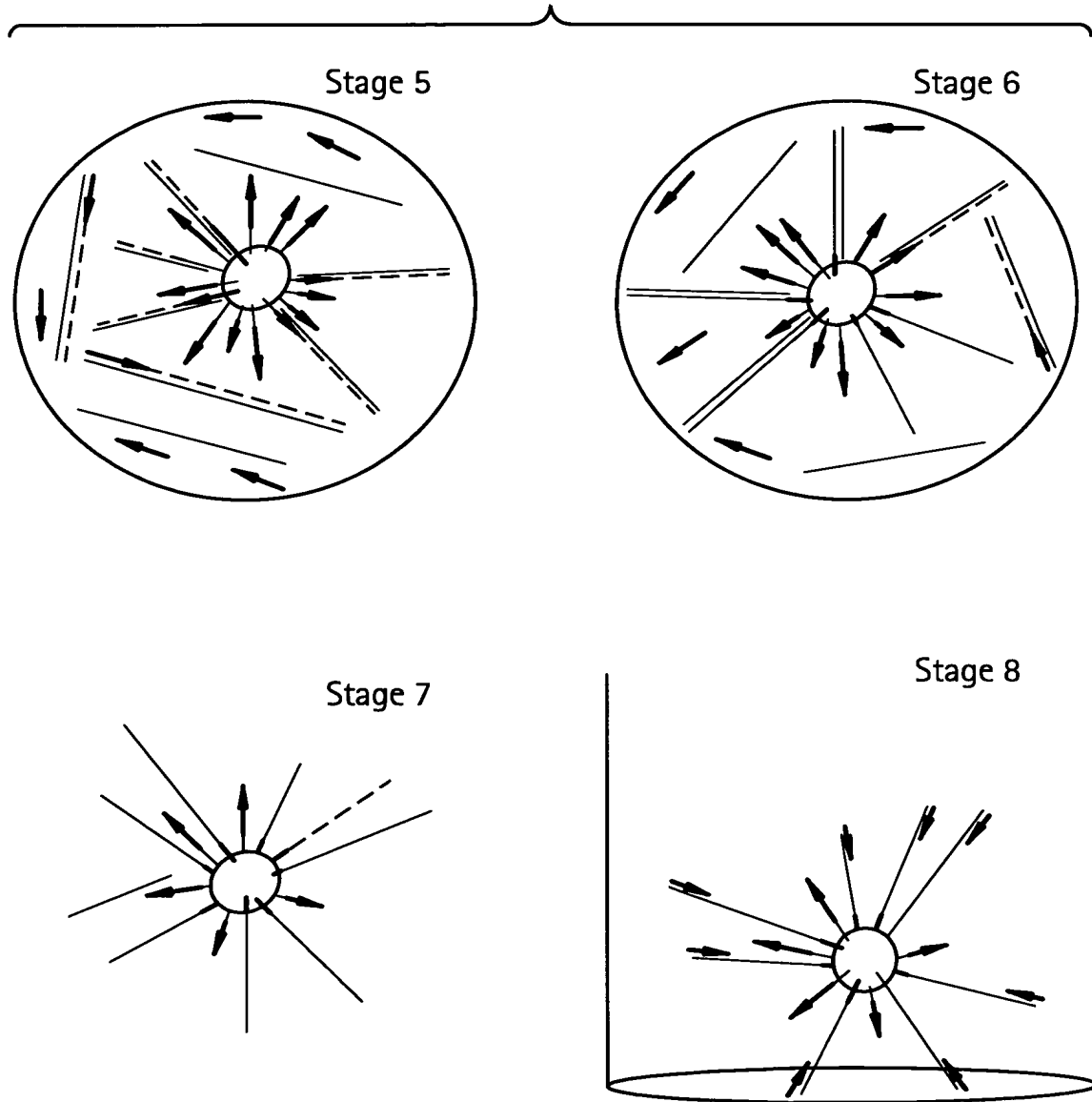


FIG. 7

Schematic Process Flow for Bead Separation

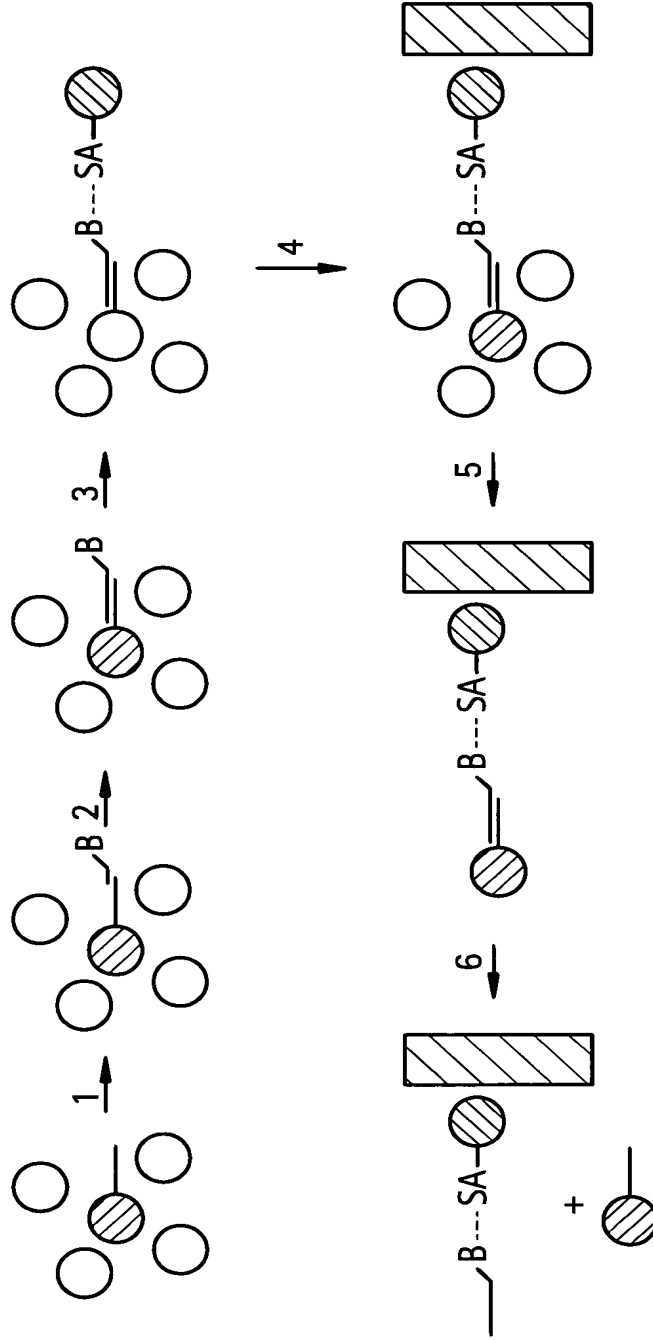


FIG. 8A

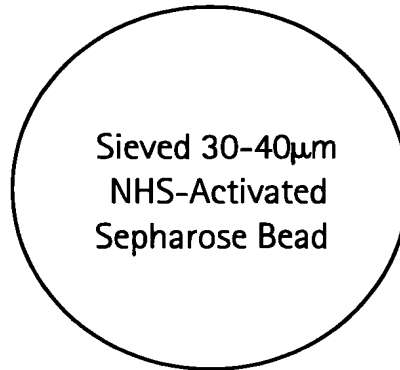


FIG. 8B

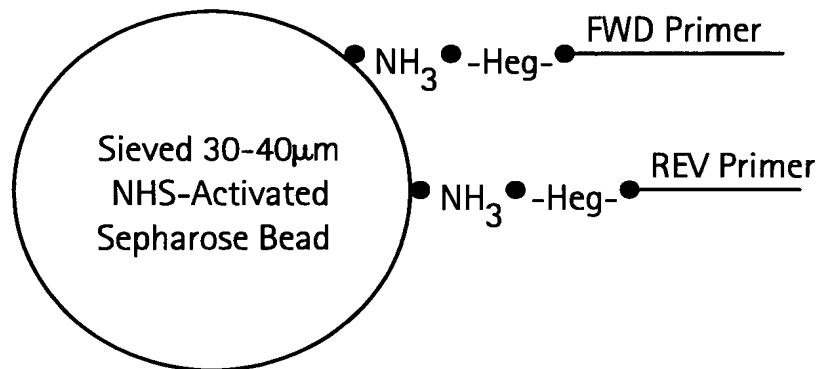


FIG. 8C

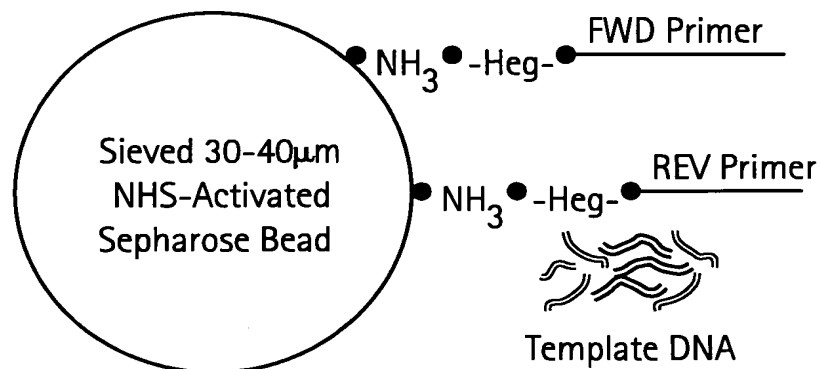


FIG. 8D

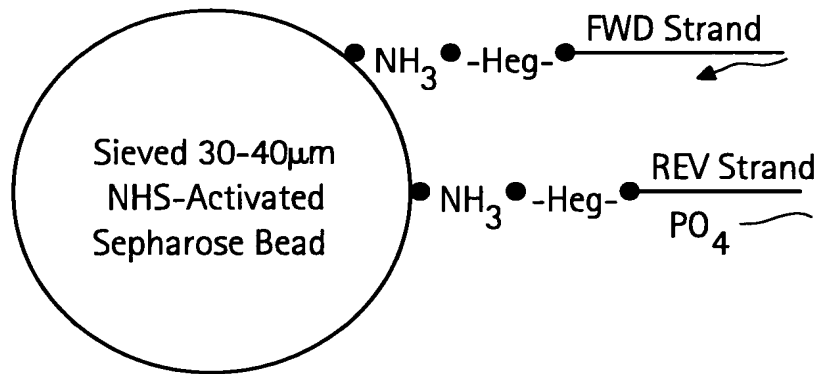


FIG. 8E

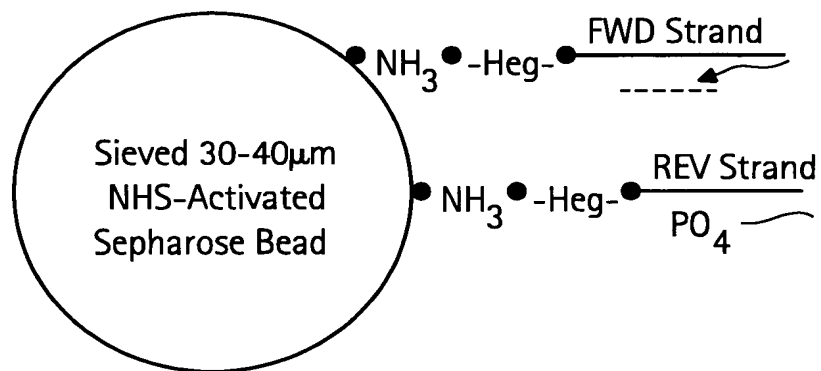


FIG. 8F

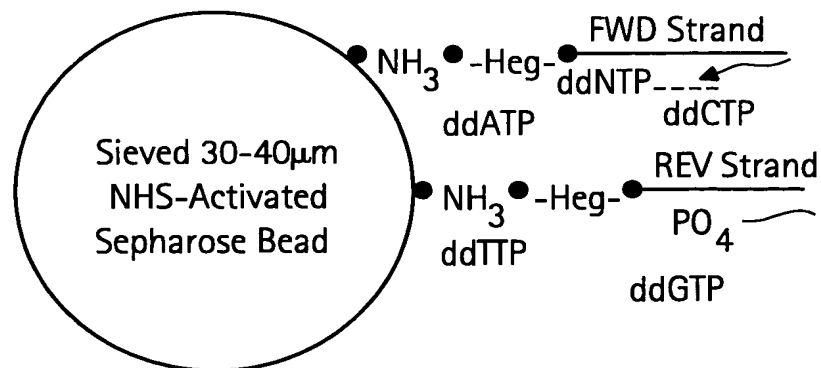


FIG. 8G

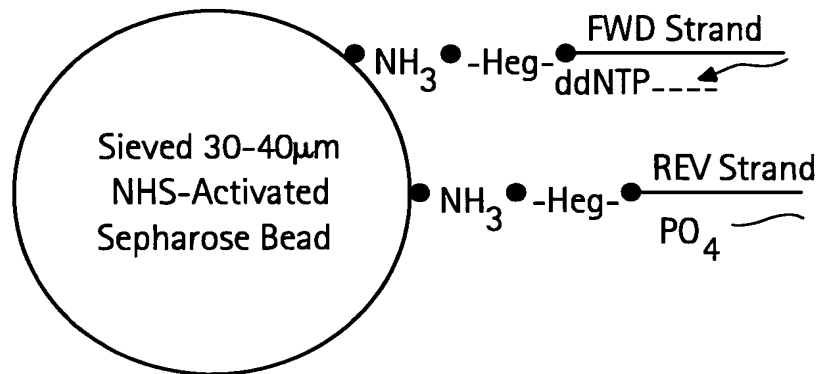


FIG. 8H

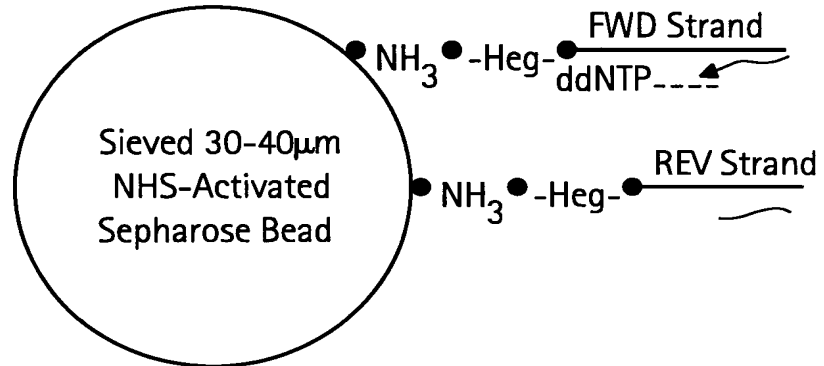


FIG. 8I

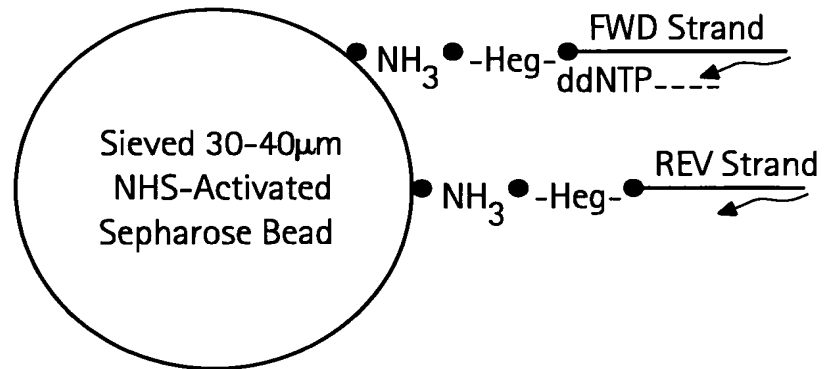


FIG. 8J

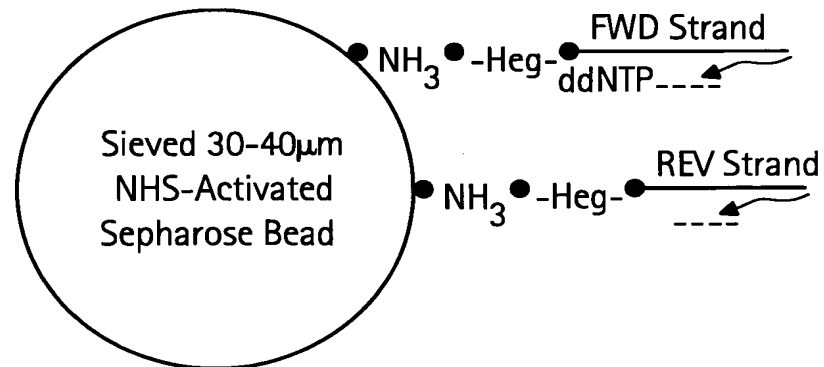


FIG. 9

1_21_03 N7 from 1_14_03 10X Double Strand

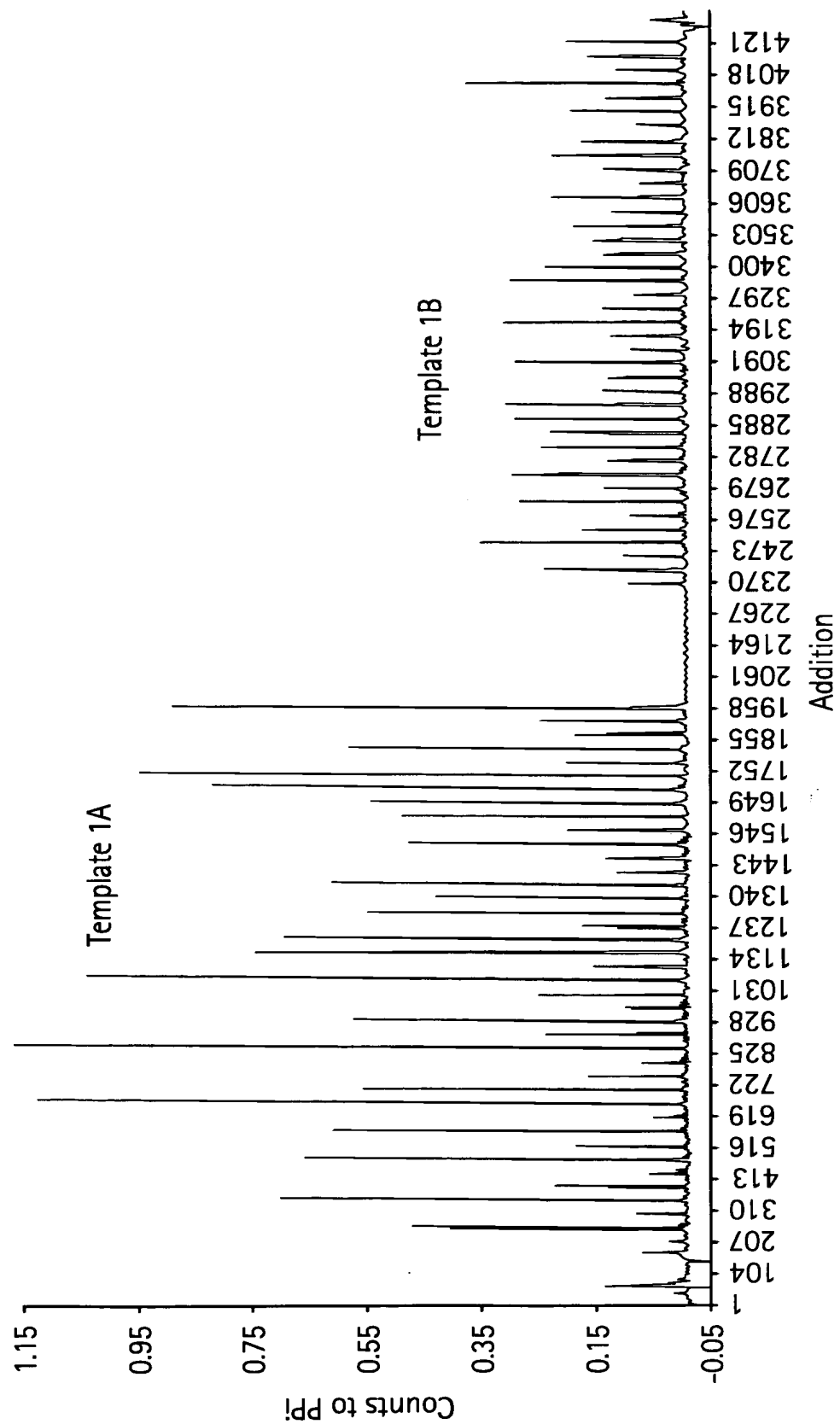


FIG. 10A

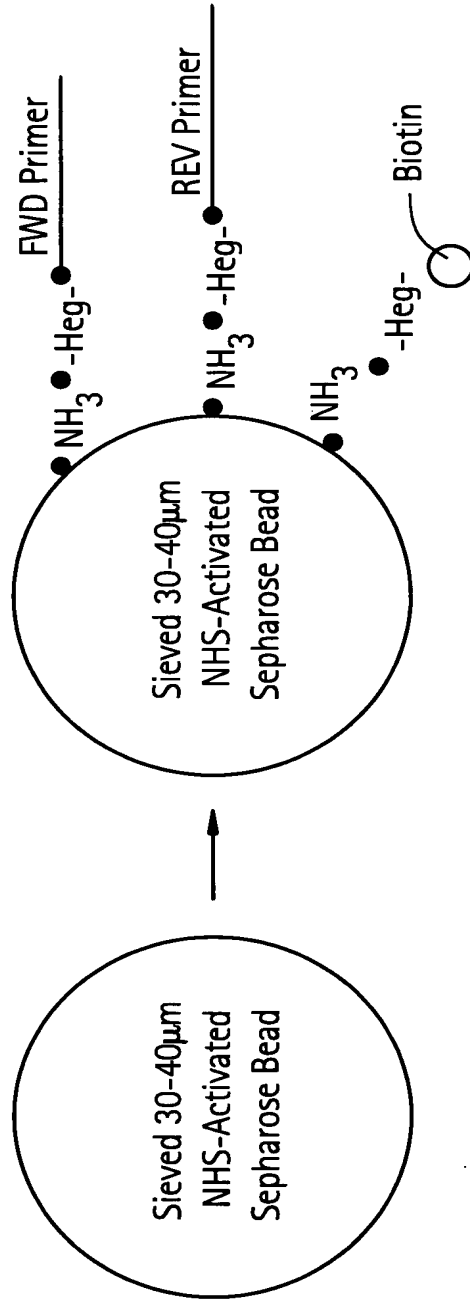


FIG. 10B

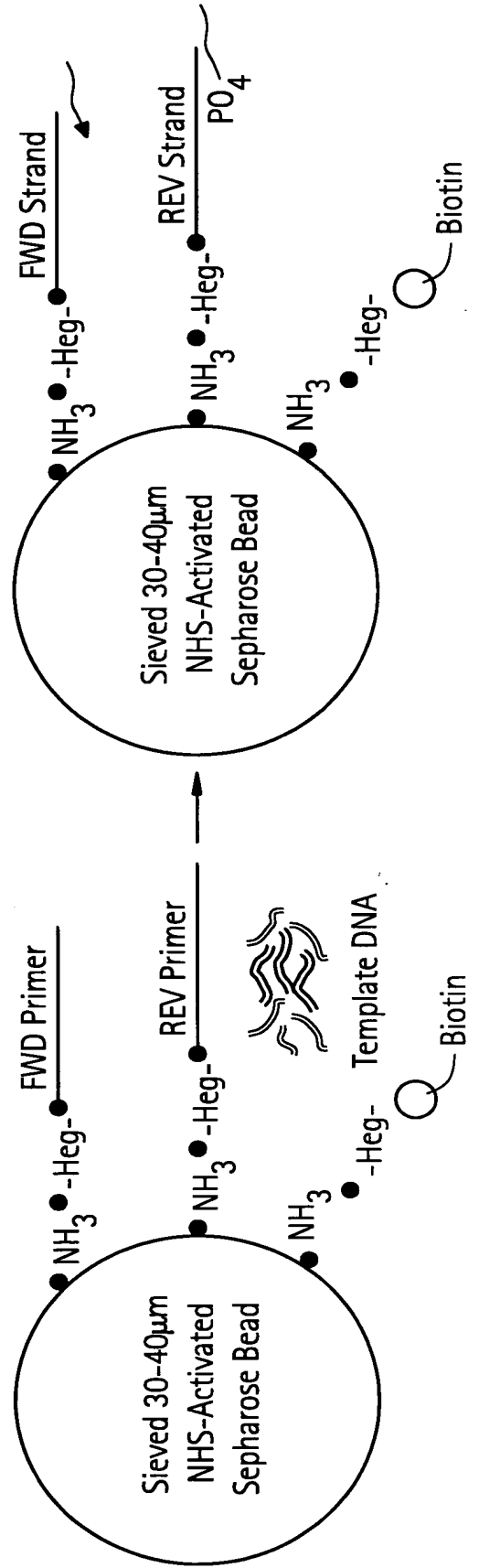


FIG. 10C

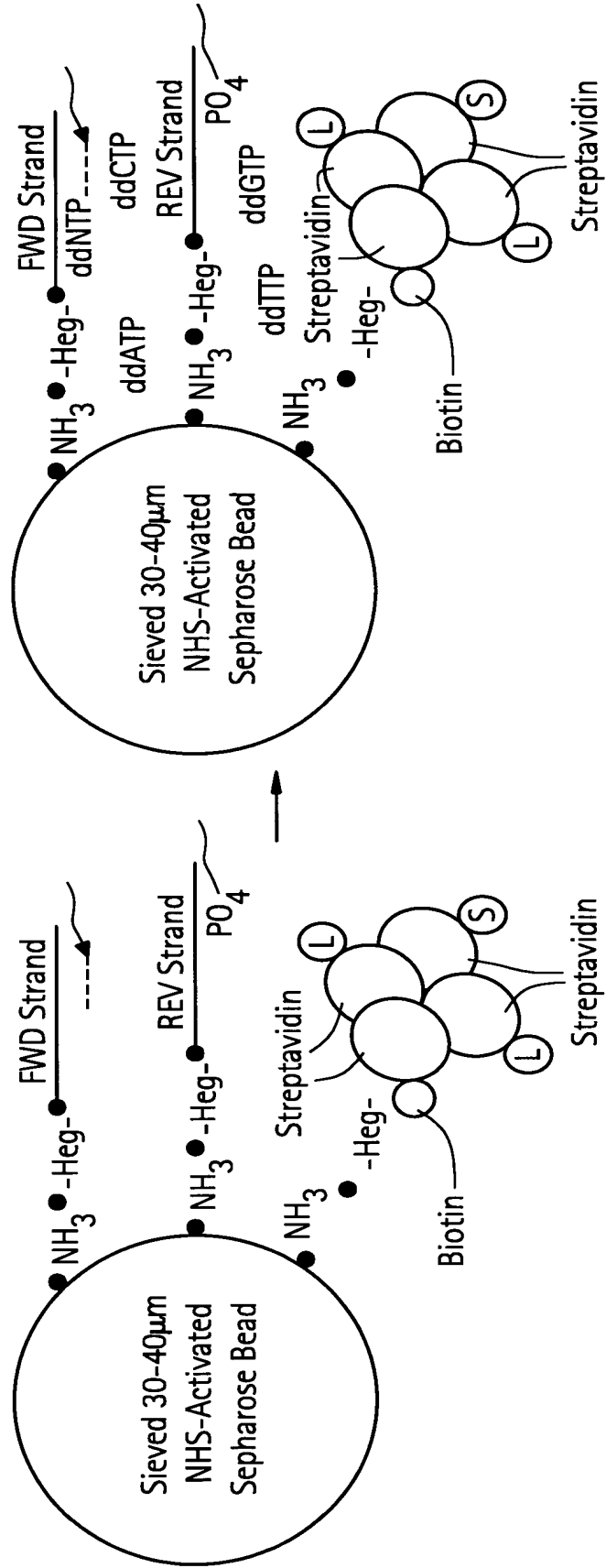


FIG. 10D

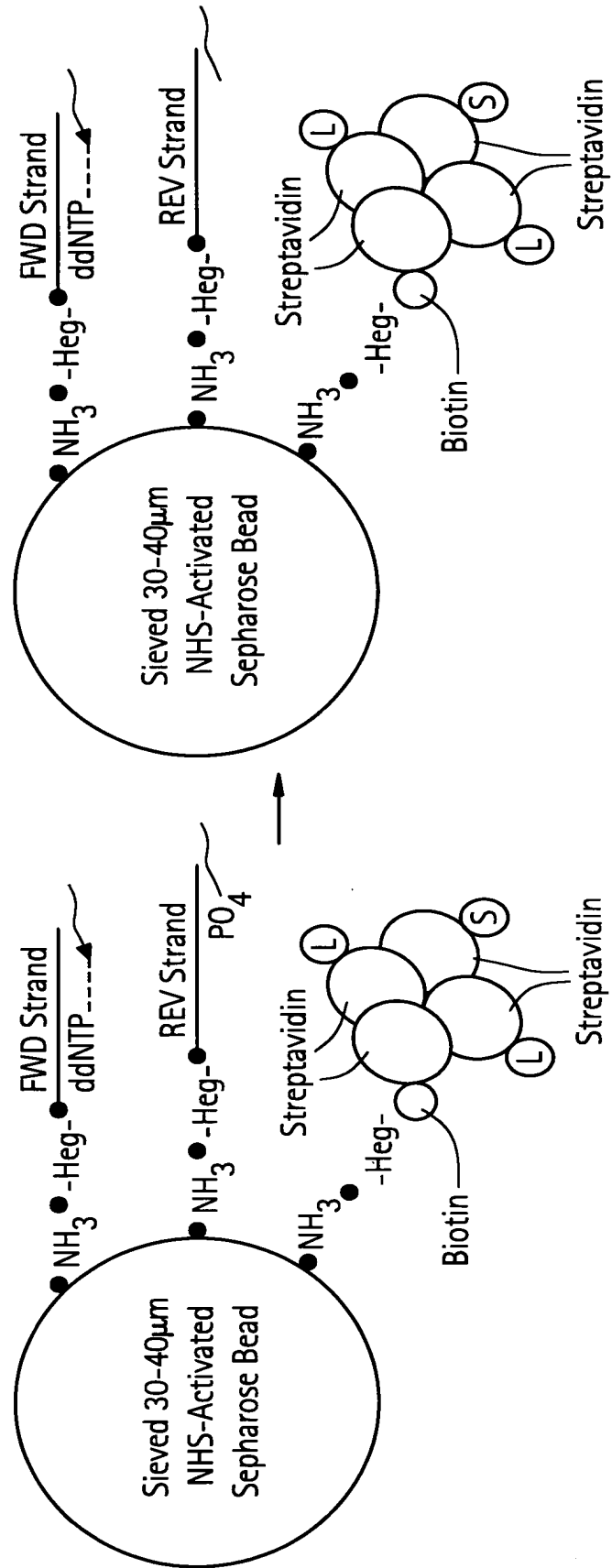
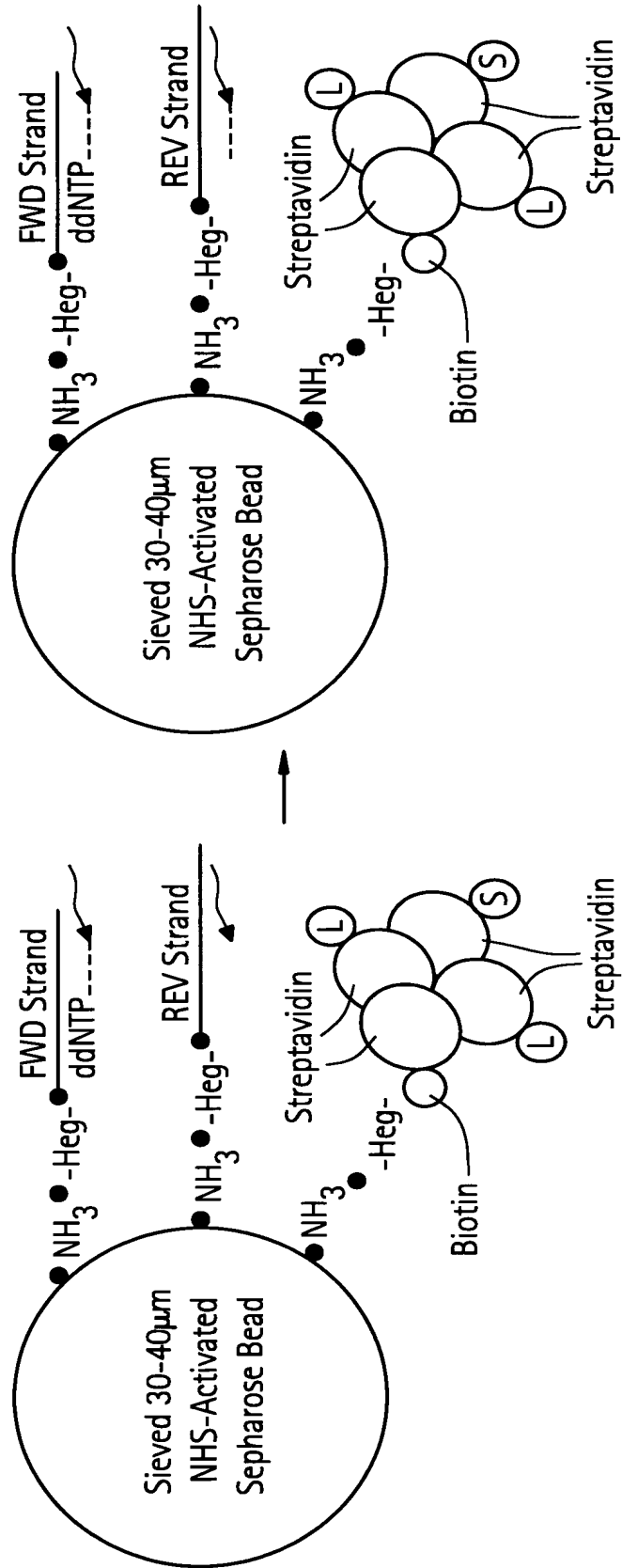
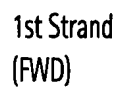


FIG. 10E





ATGC ACATGGTTGACACAGTGG

ATGC CACCGACCTAGTCTCAACTT

2nd Strand
(REV)

Sample	Well Location	Sequence	Perfect Match Length
F6_14_1	00003_1363_1660.well	ATGCCACCGACCTAGTCTCAAACIT	25

FIG. 11A

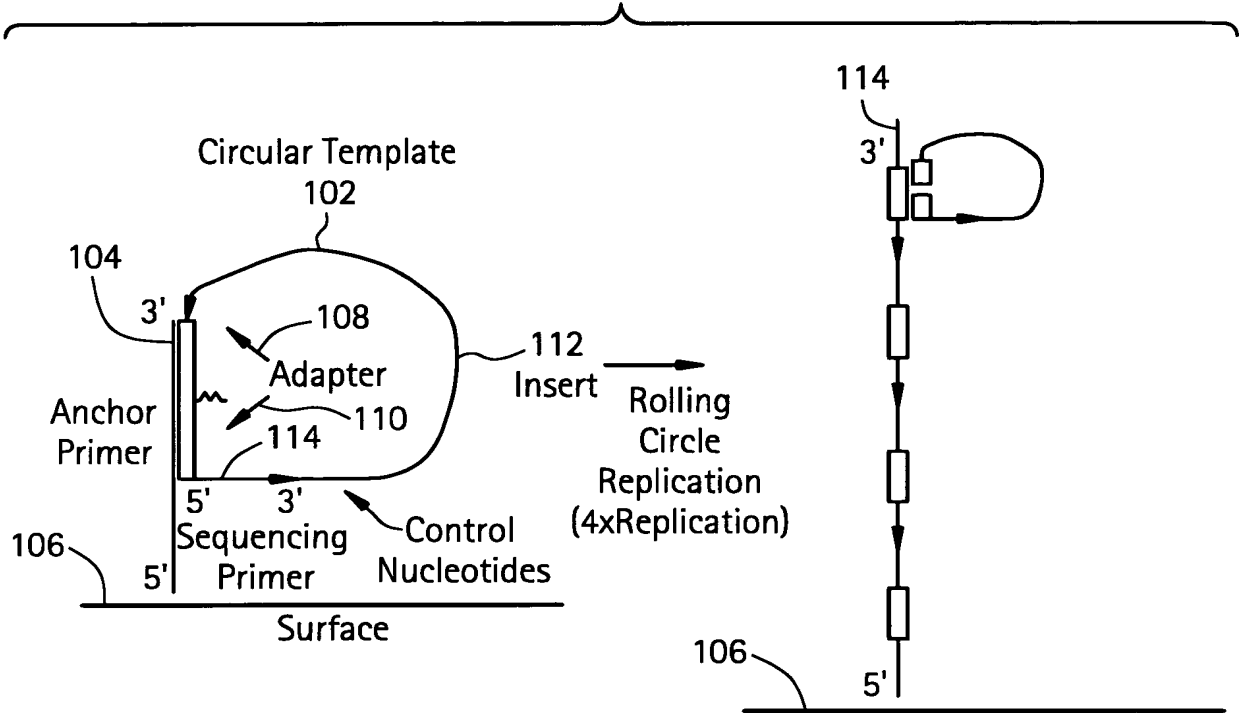


FIG. 11B

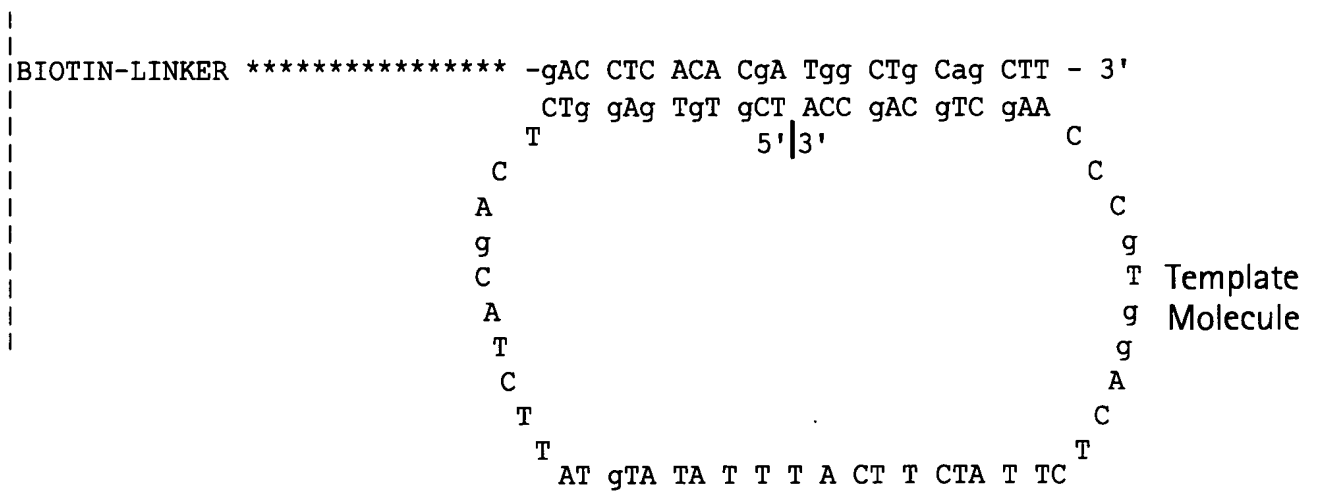


FIG. 11C

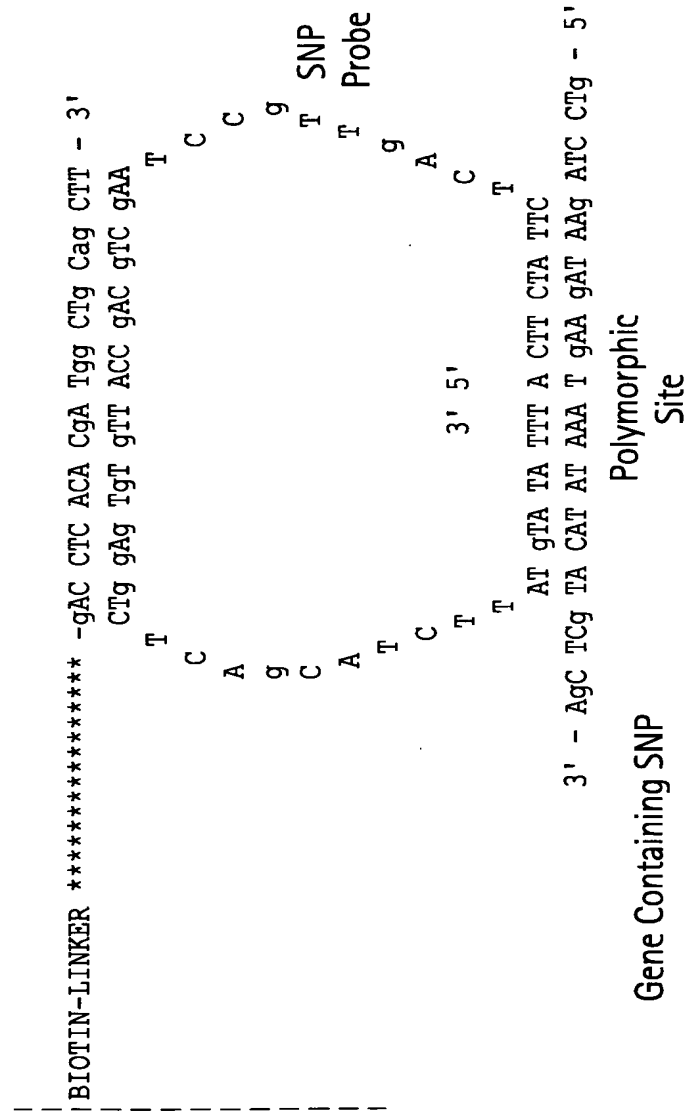


FIG. 11D

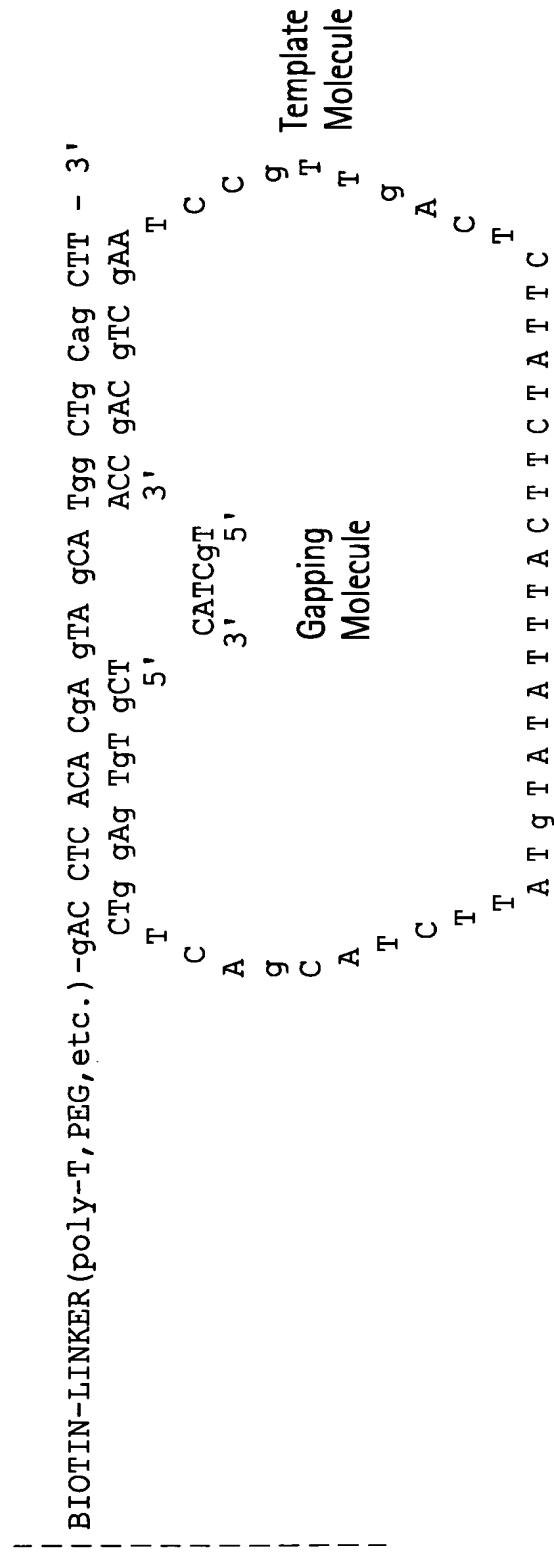


FIG. 12

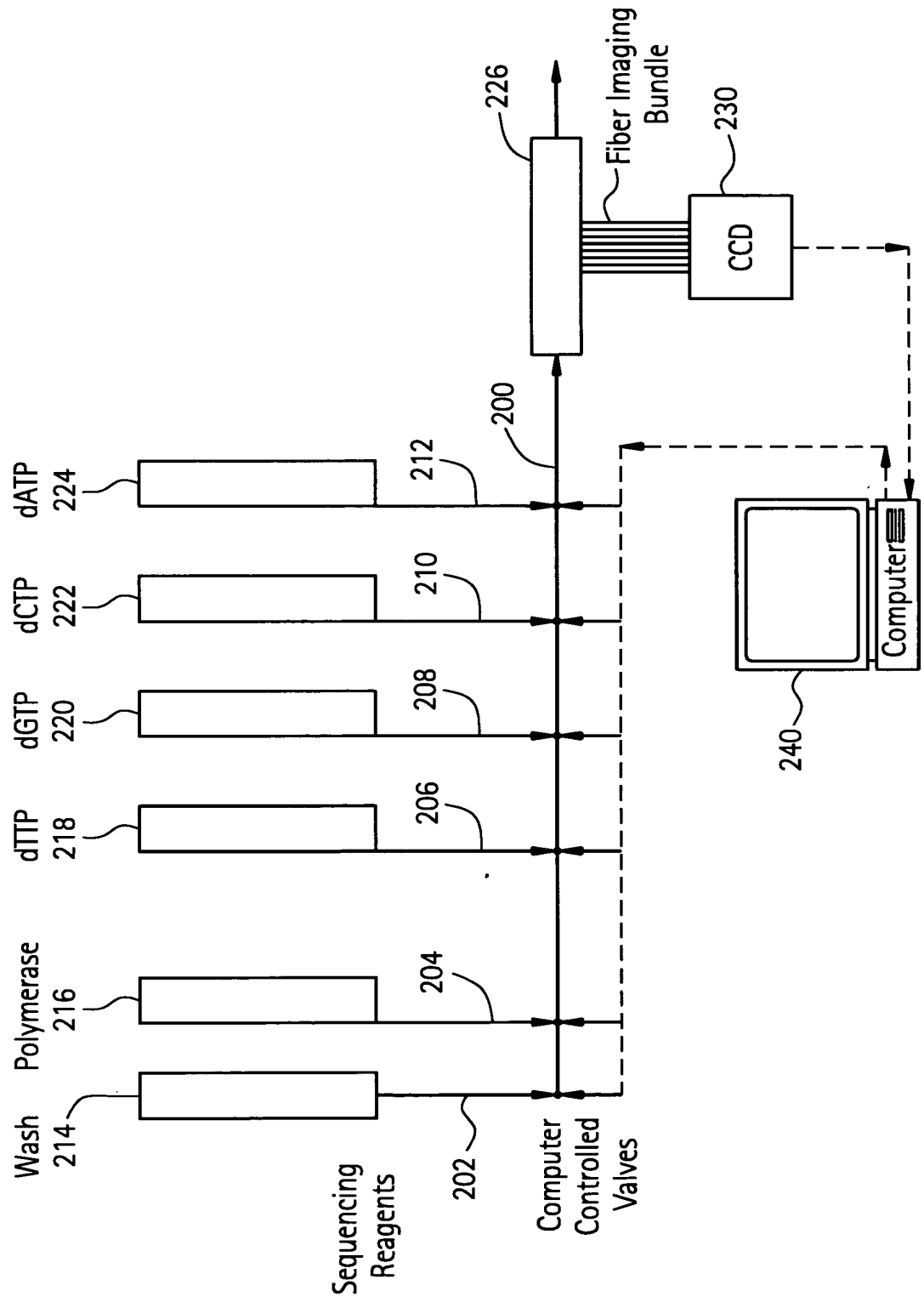


FIG. 13

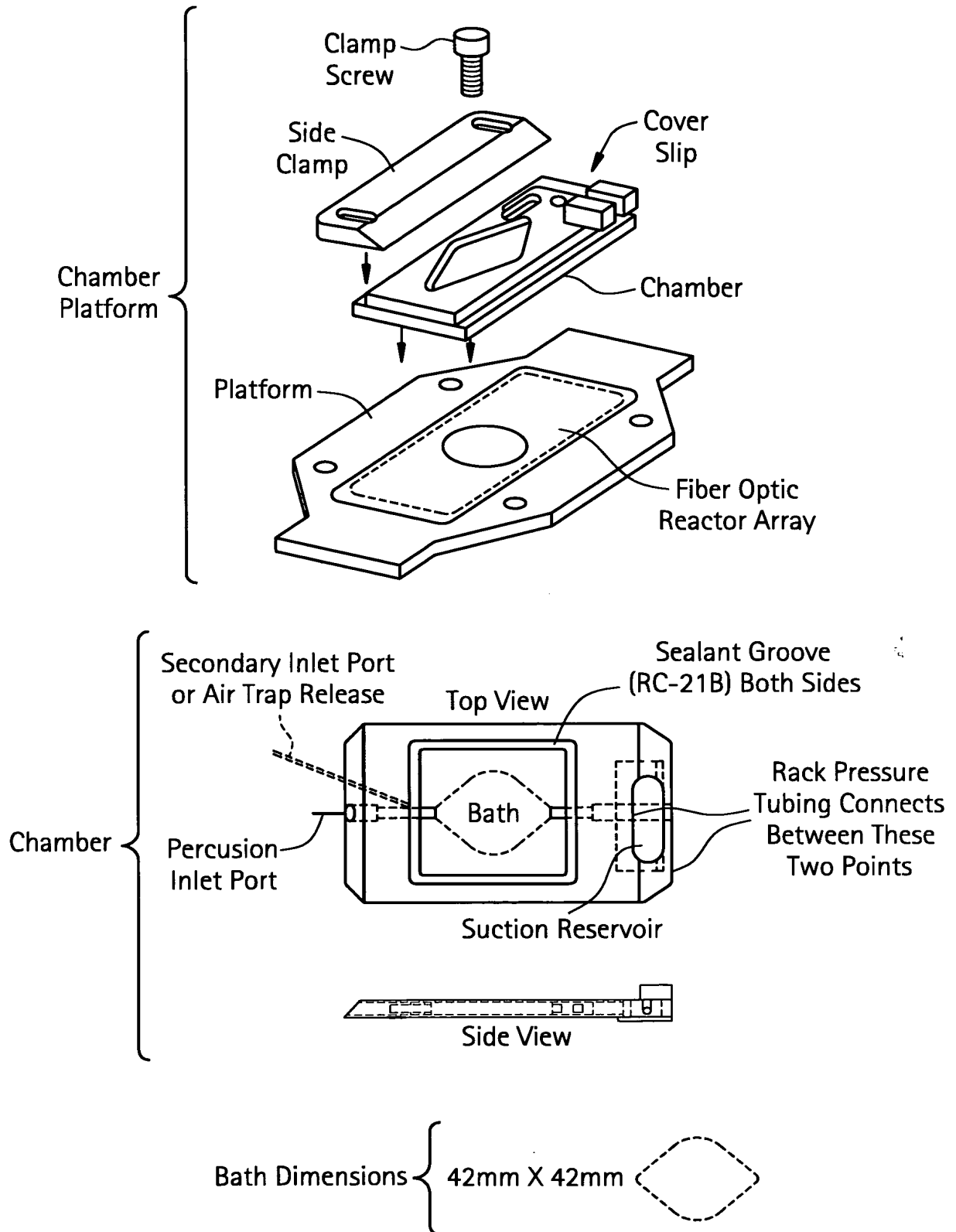


FIG. 14

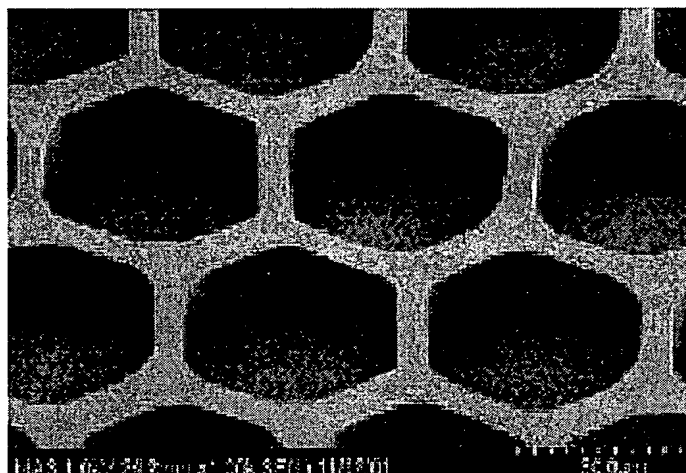
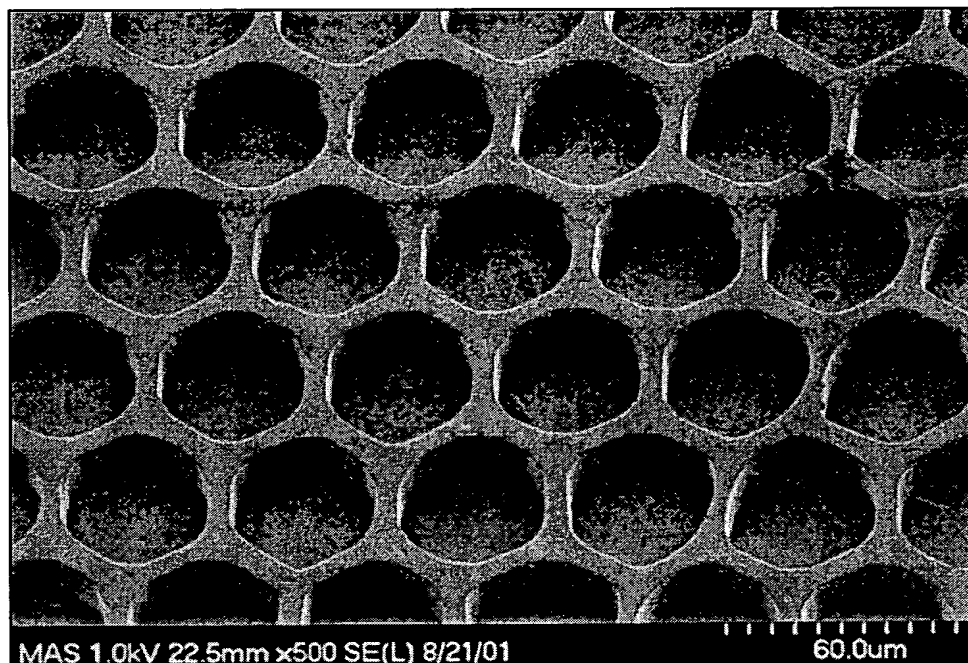


FIG. 15

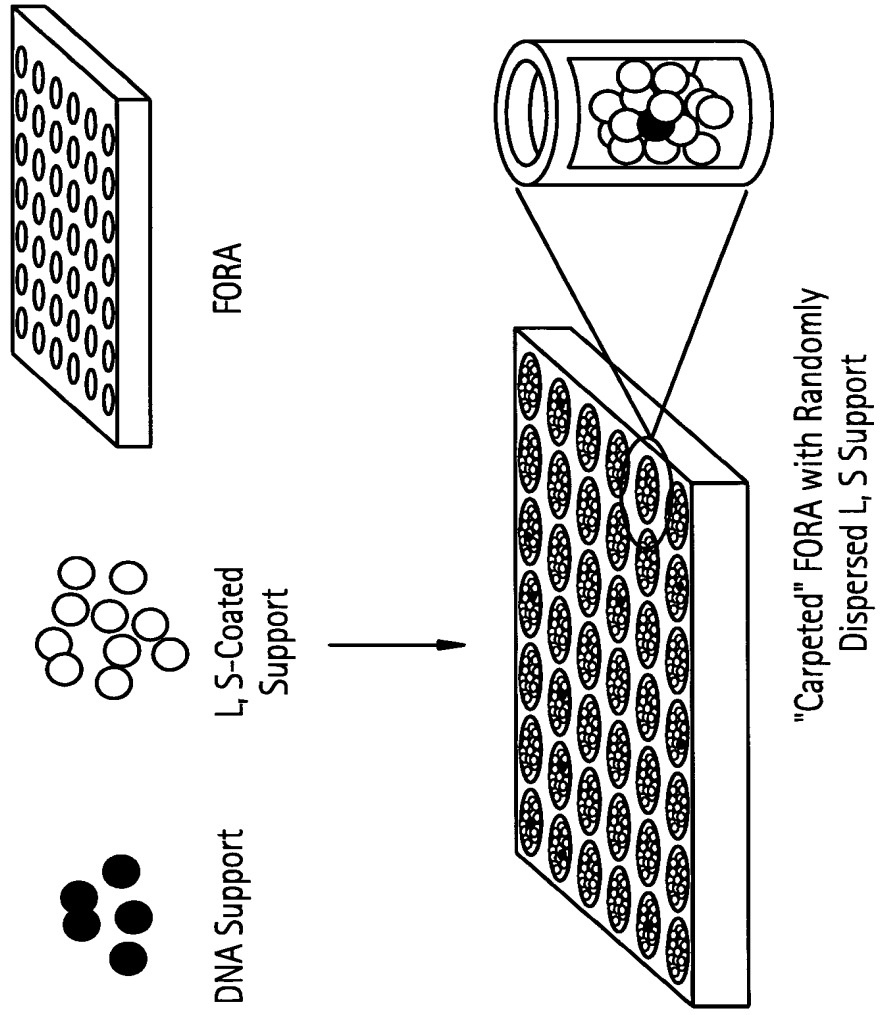


FIG. 16

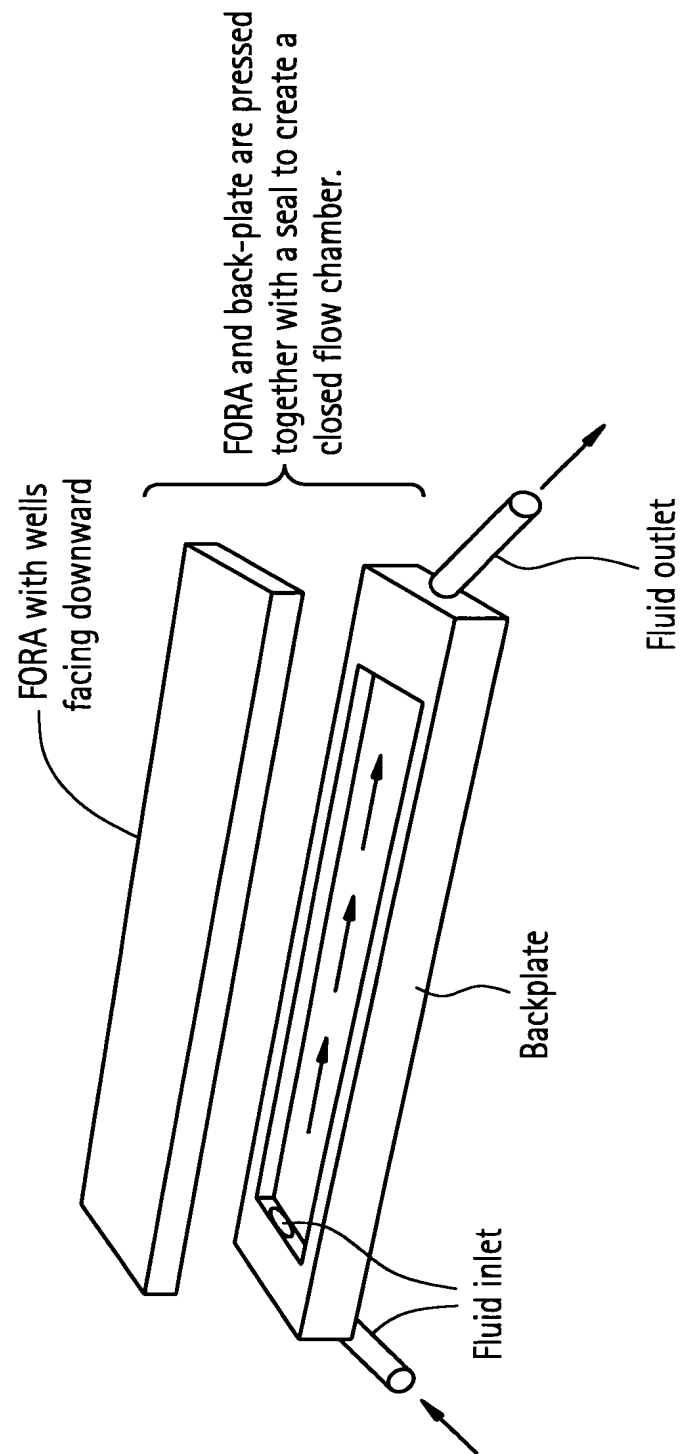


FIG. 17

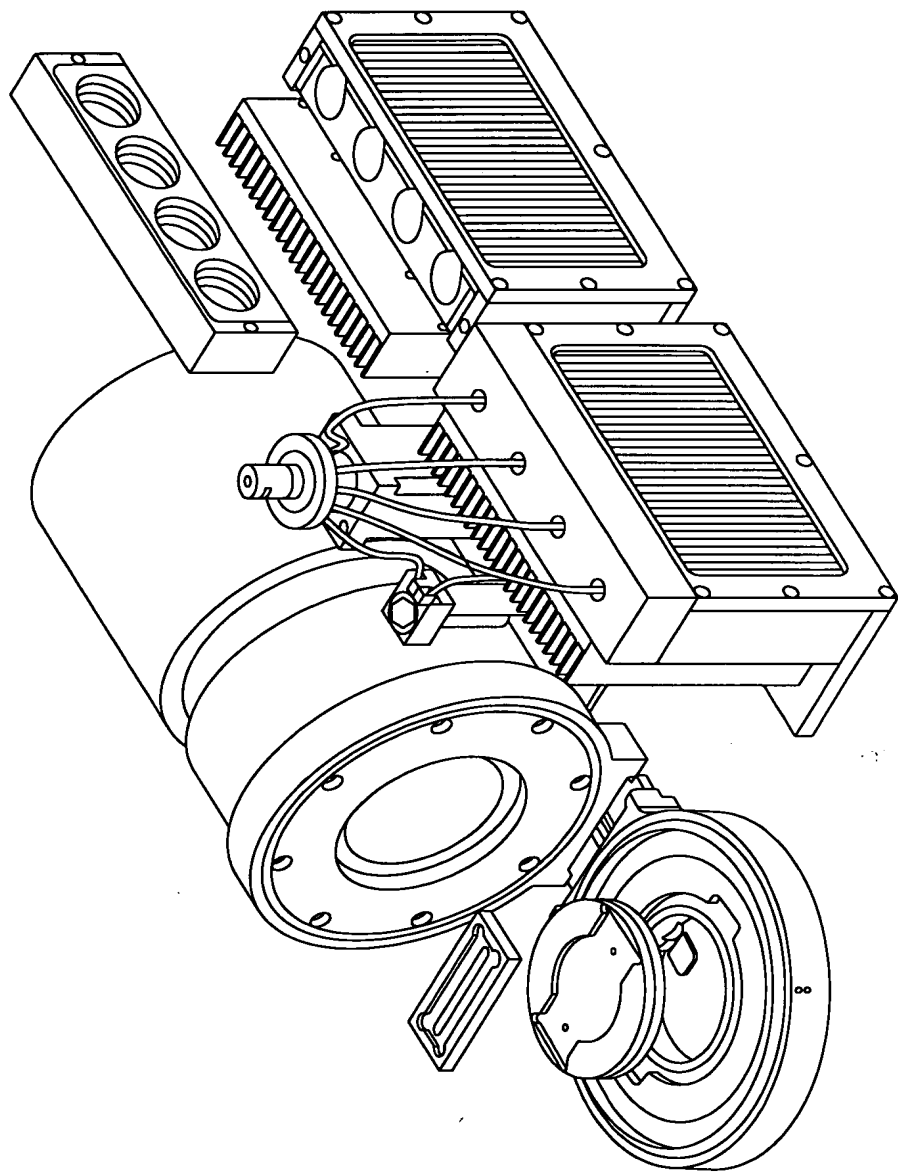


FIG. 18

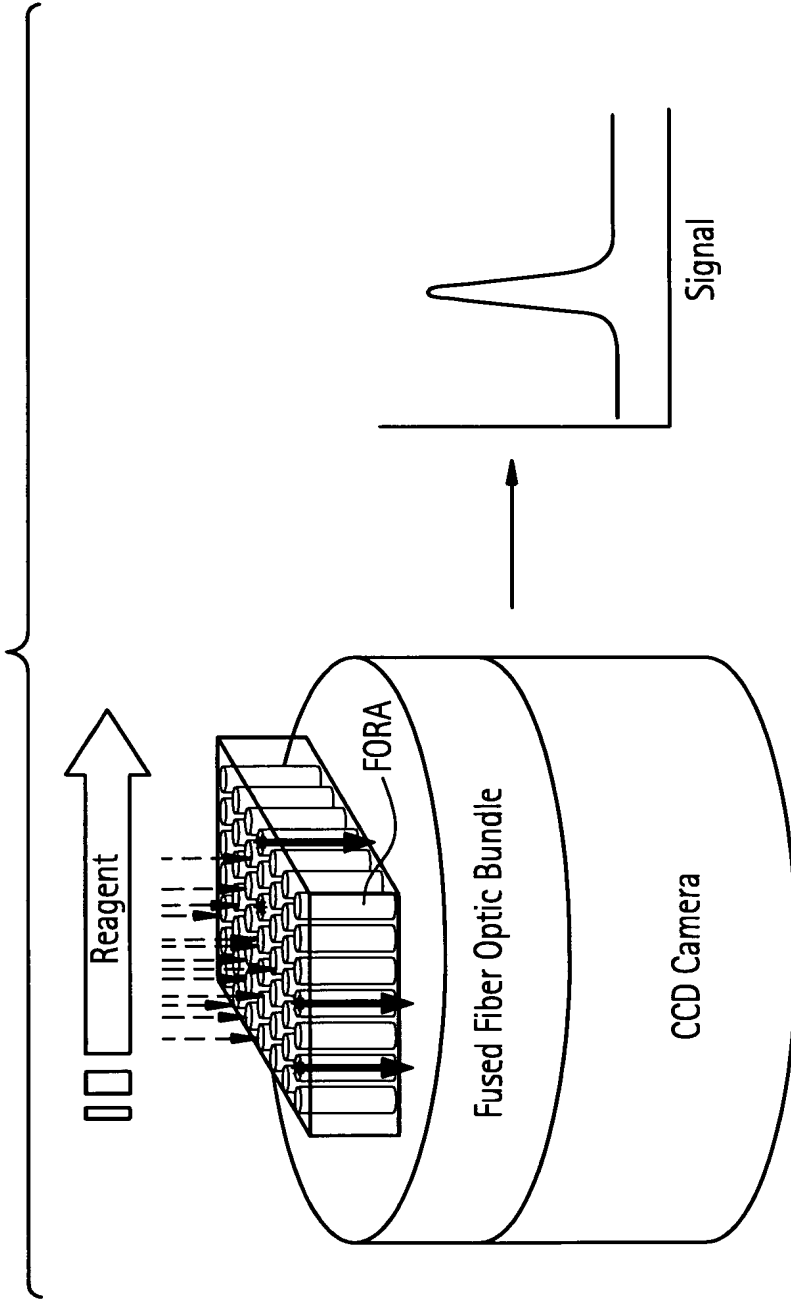


FIG. 19

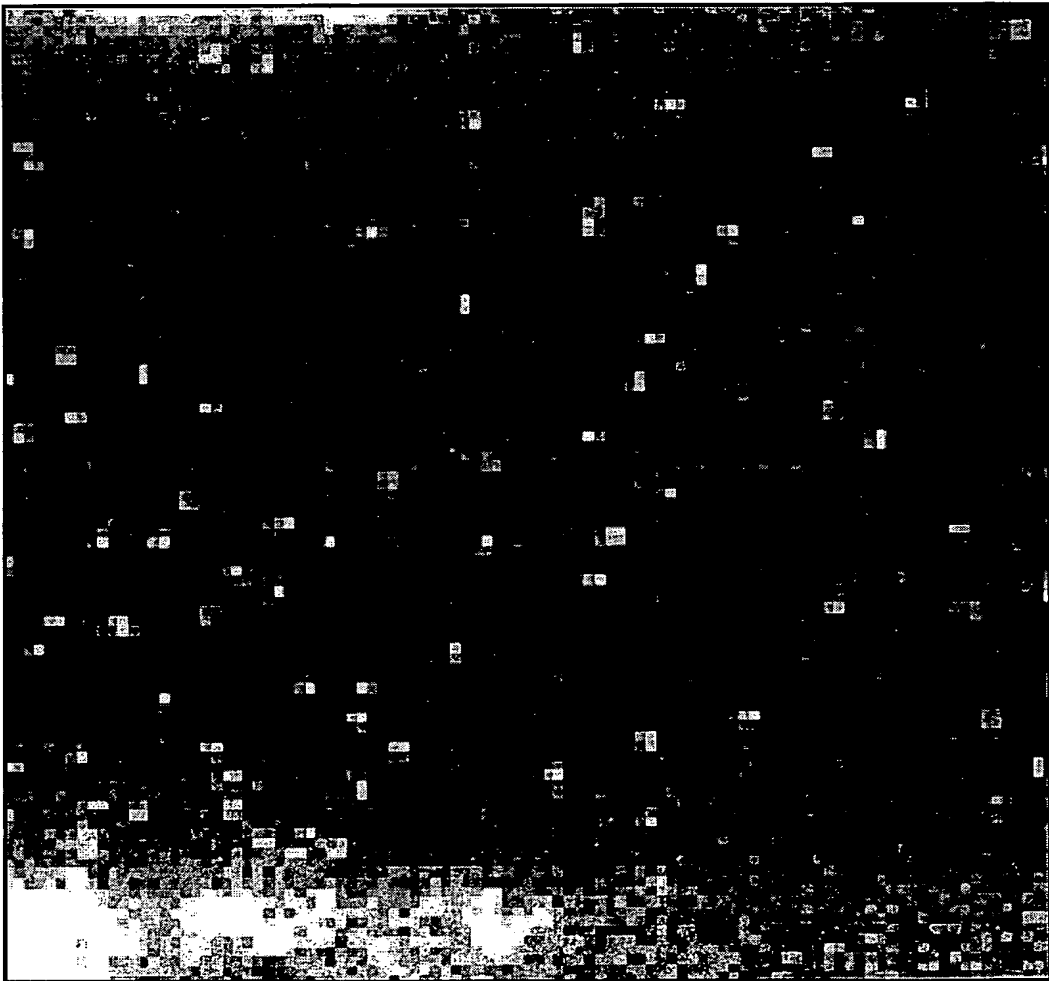


FIG. 20

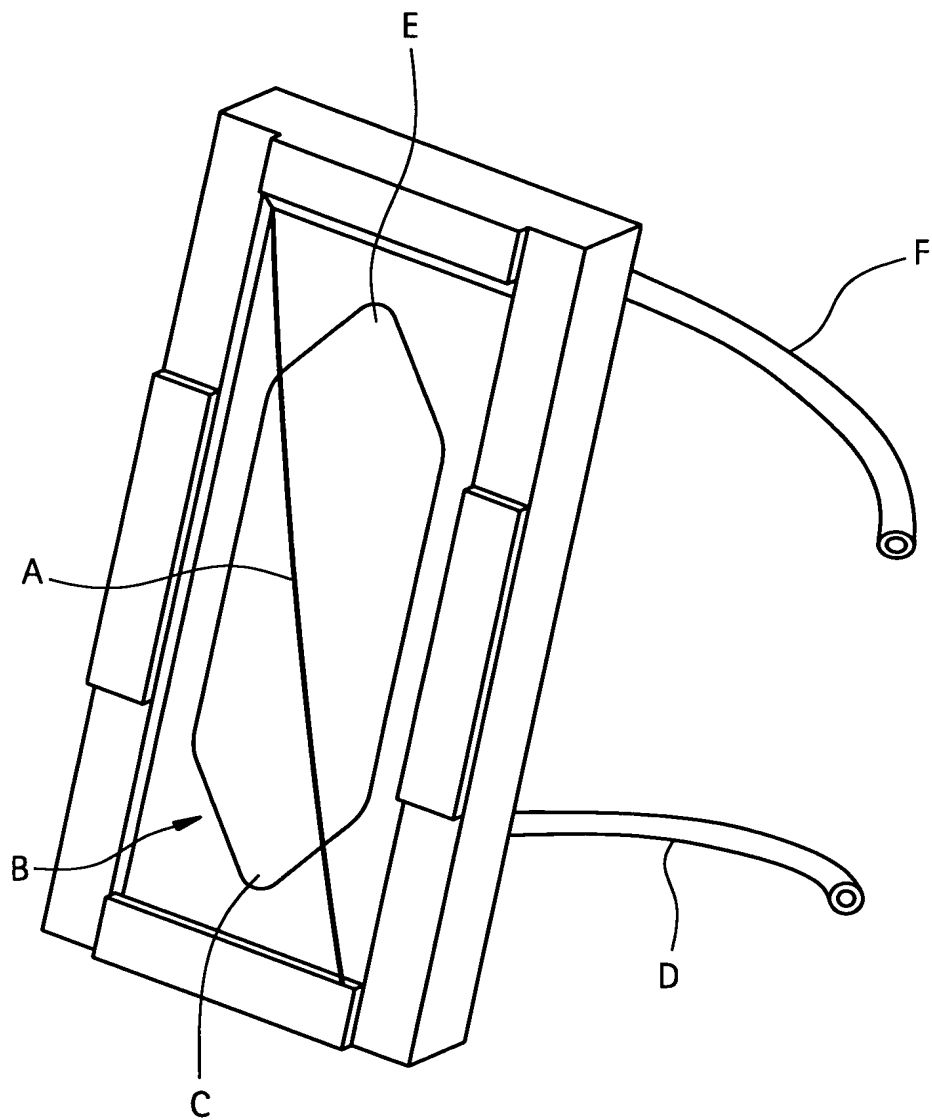


FIG. 21

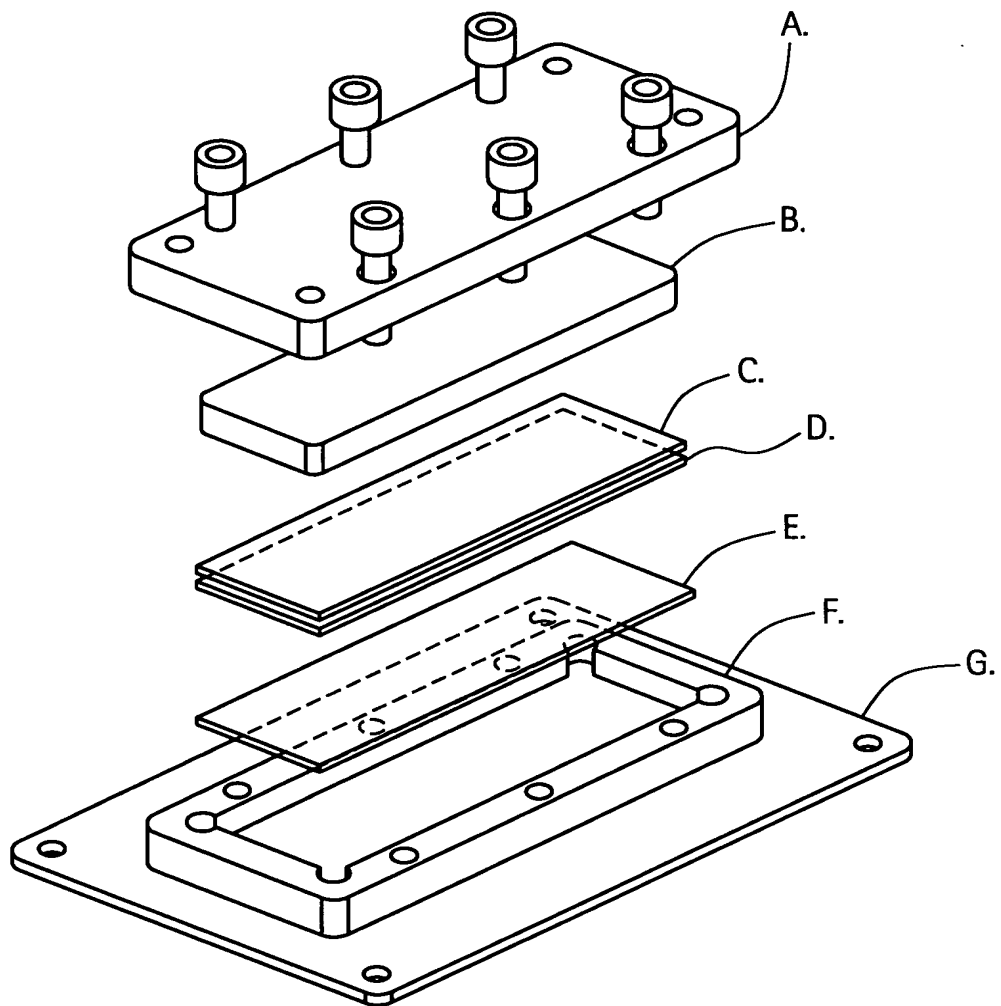


FIG. 22

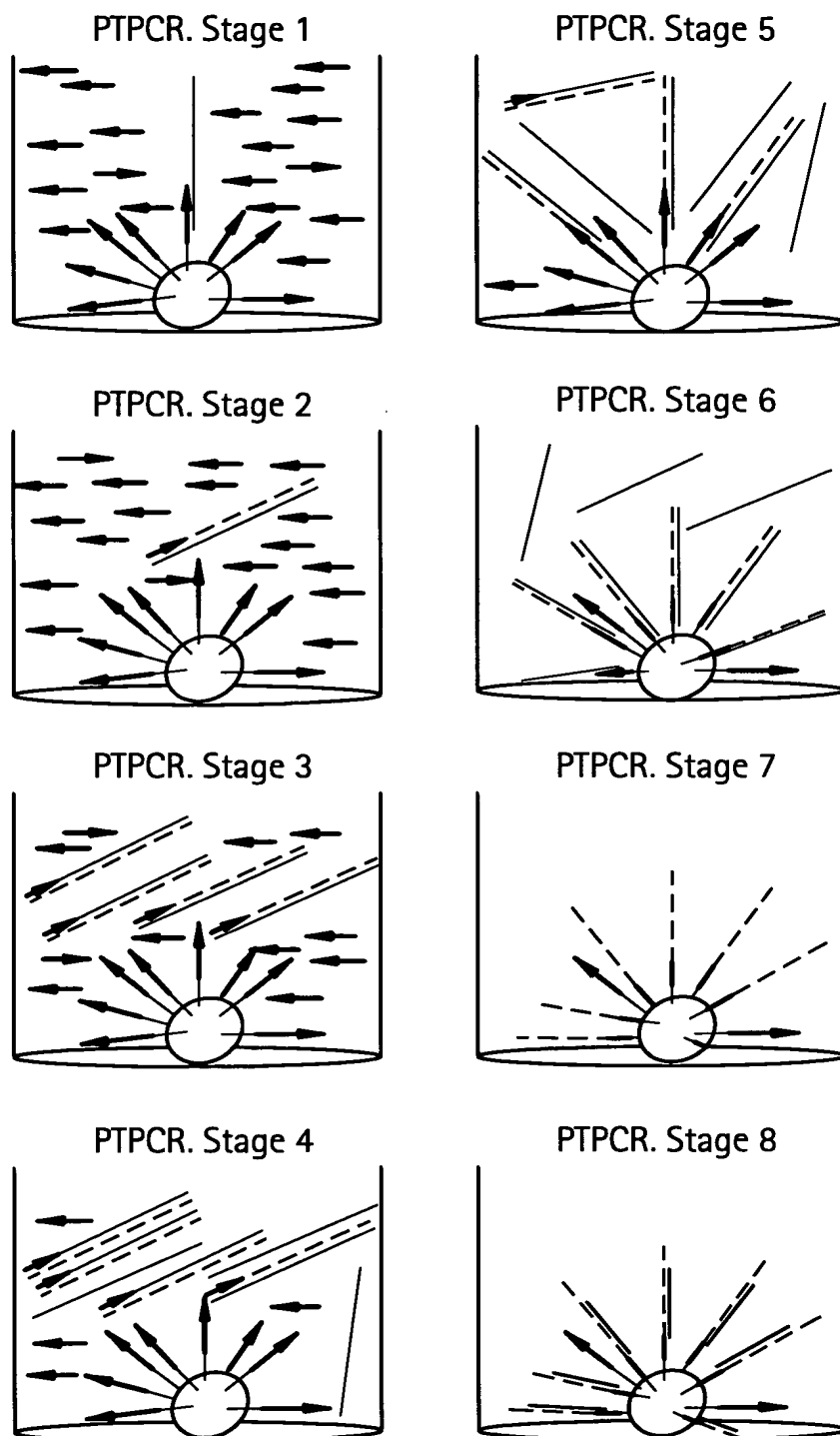


FIG. 23A

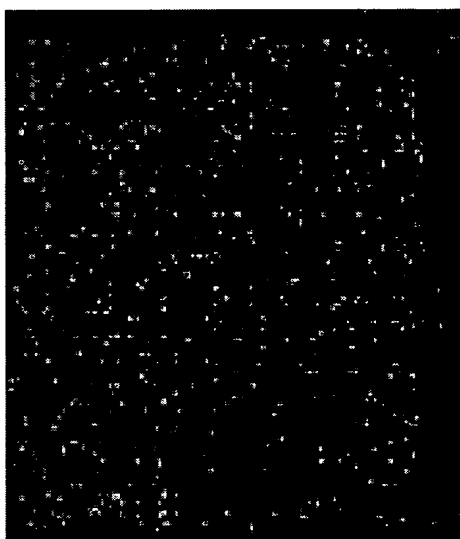


FIG. 23B

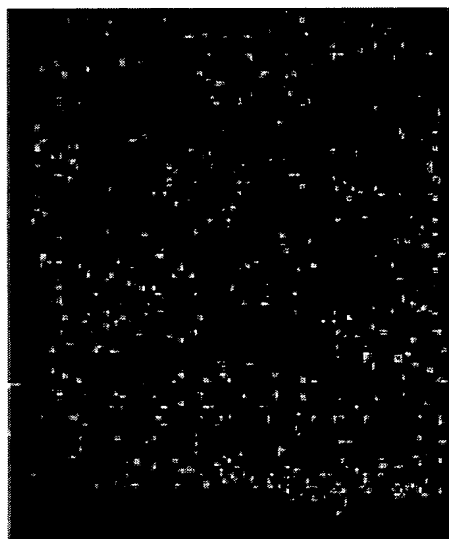


FIG. 23C



FIG. 24

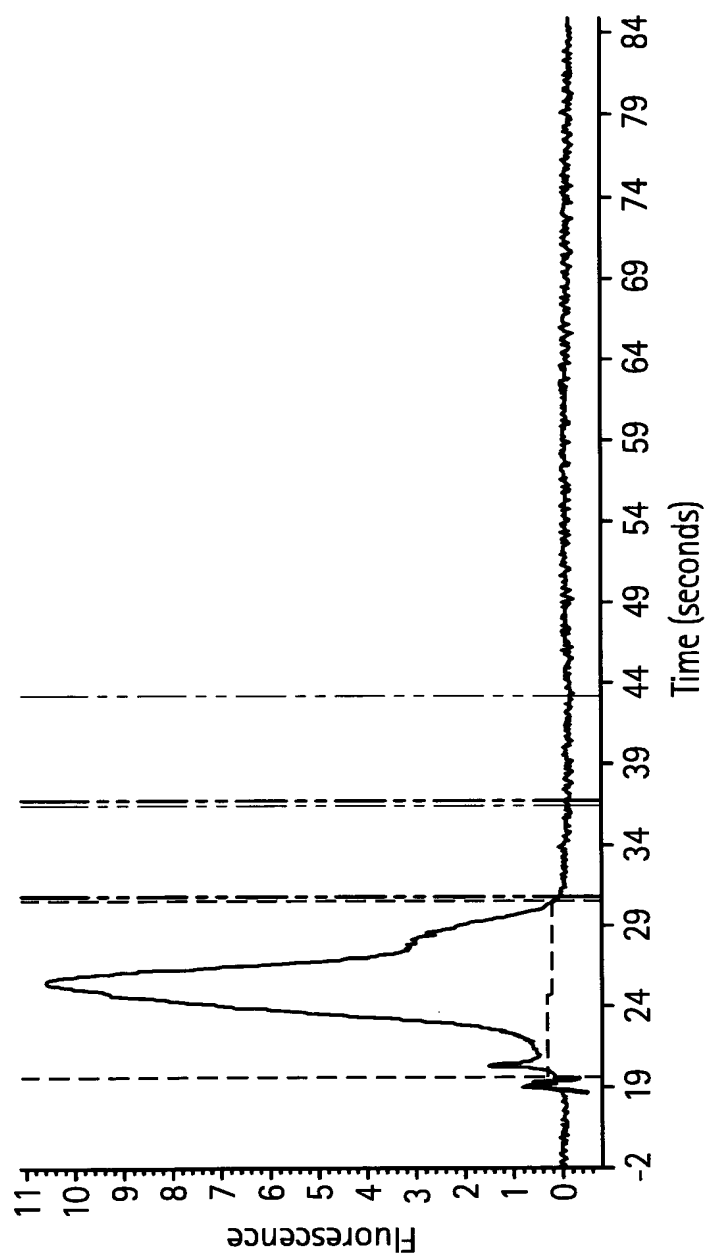


FIG. 25

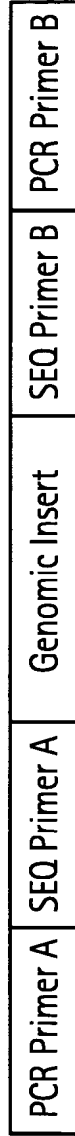


FIG. 26

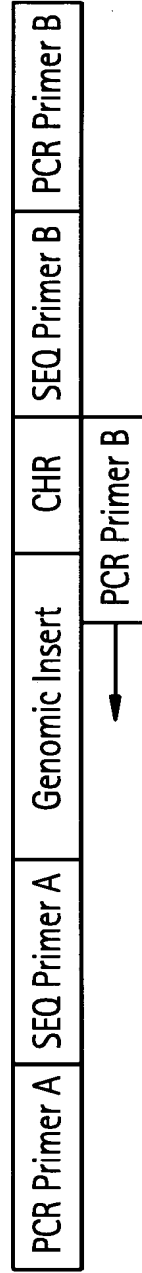


FIG. 27

Primer Candidates by T_m
8x19x19x19x9 tetrads (493,848 total possibilities)

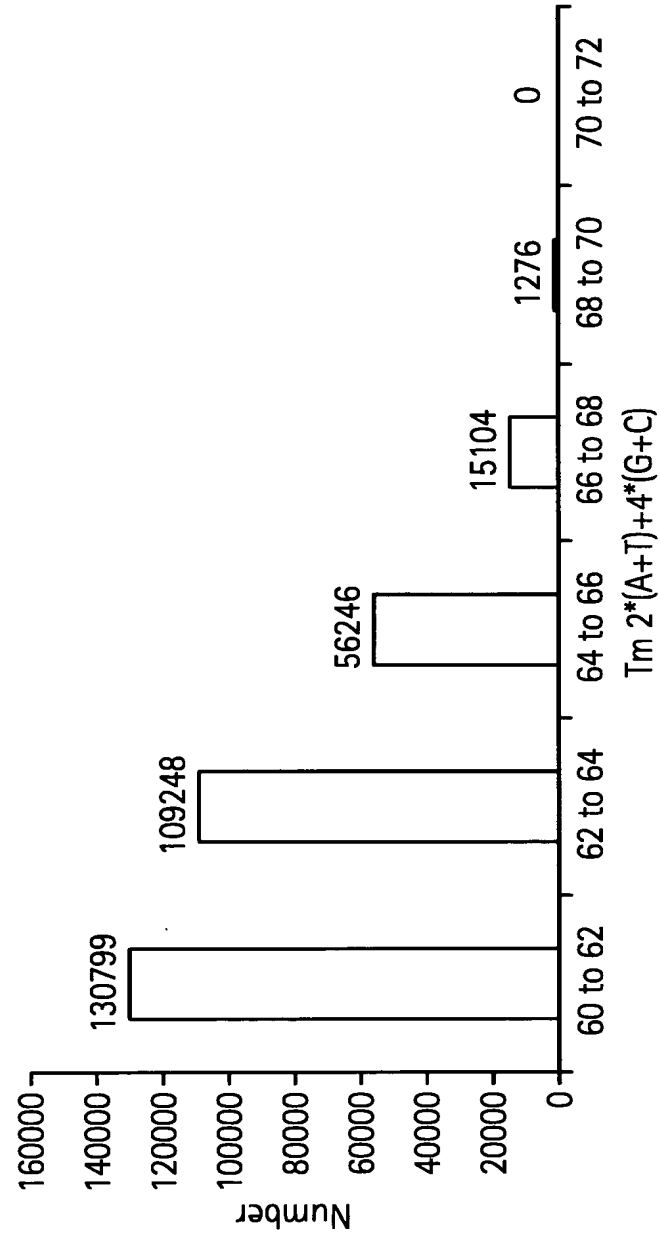


FIG. 28A



FIG. 28B



FIG. 28C

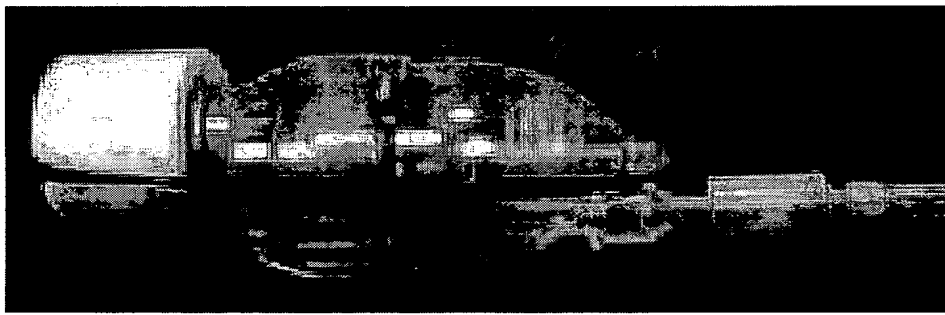


FIG. 28D

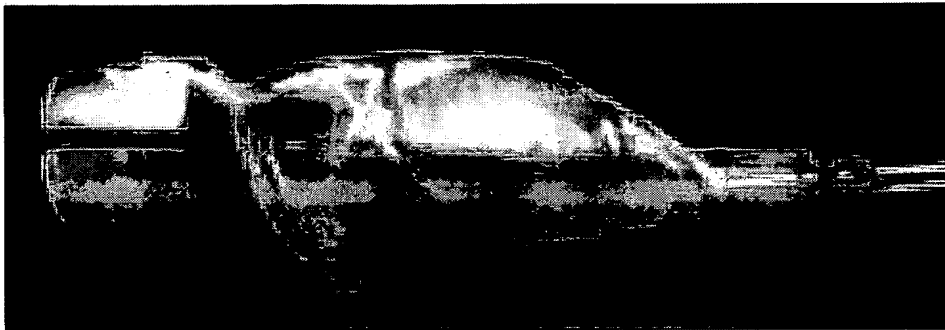


FIG. 29A

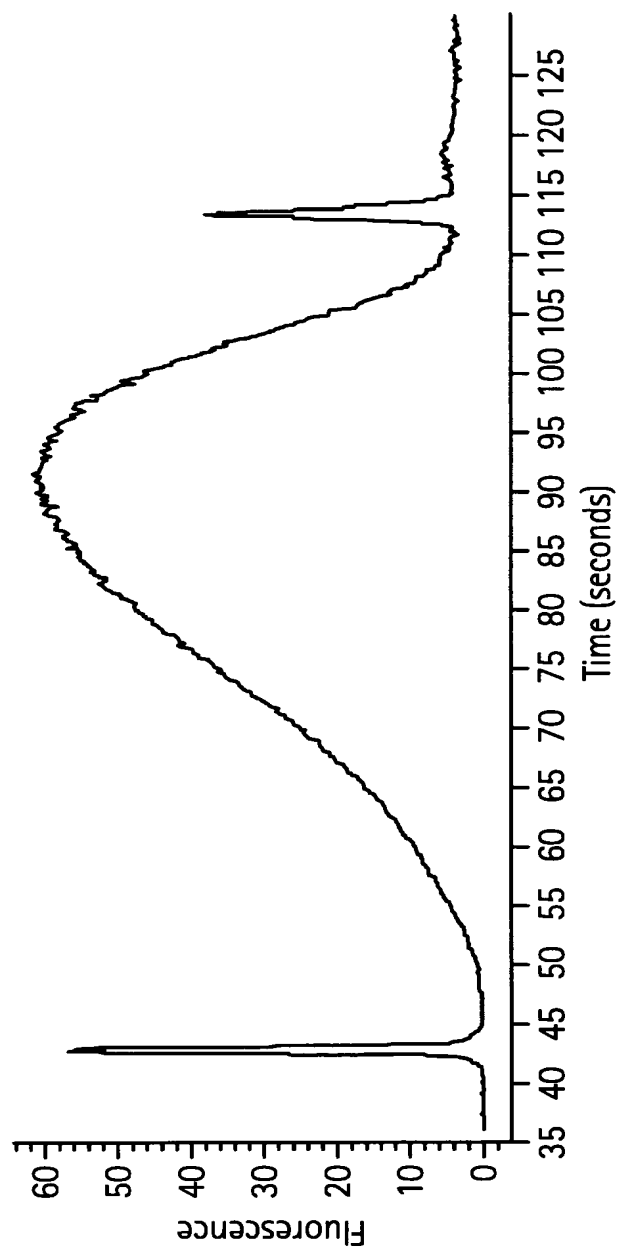


FIG. 29B

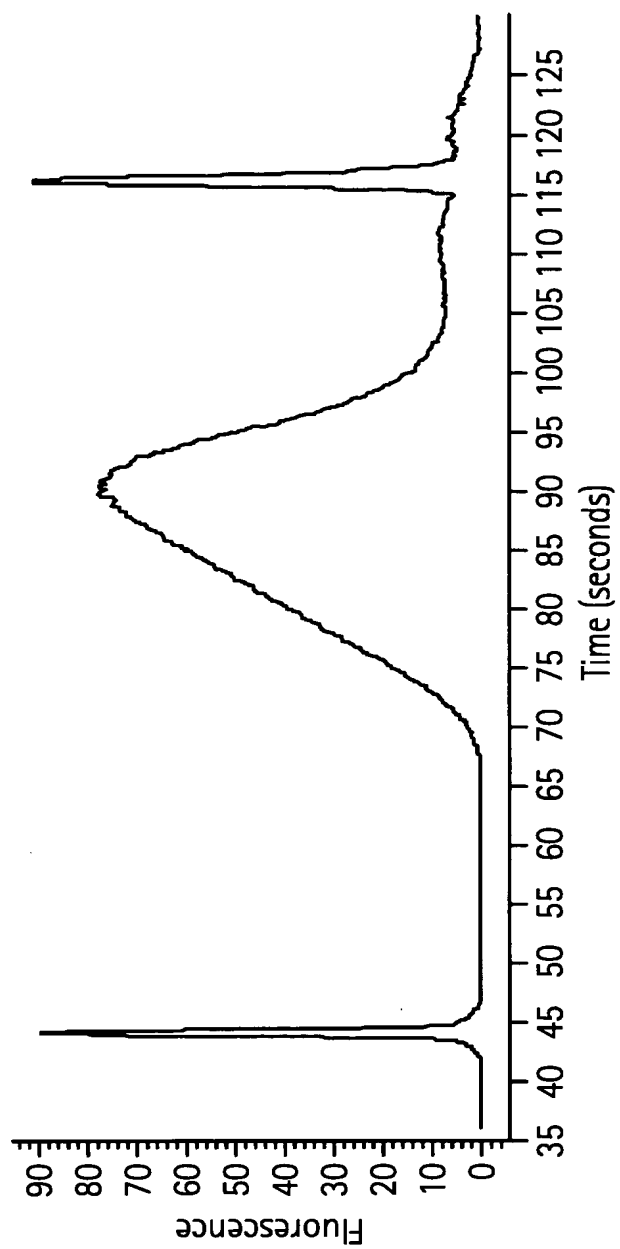


FIG. 30

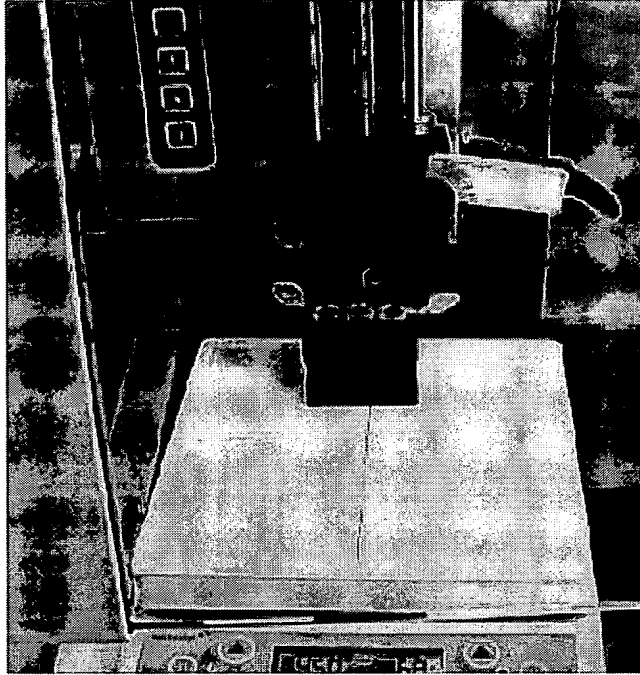


FIG. 31

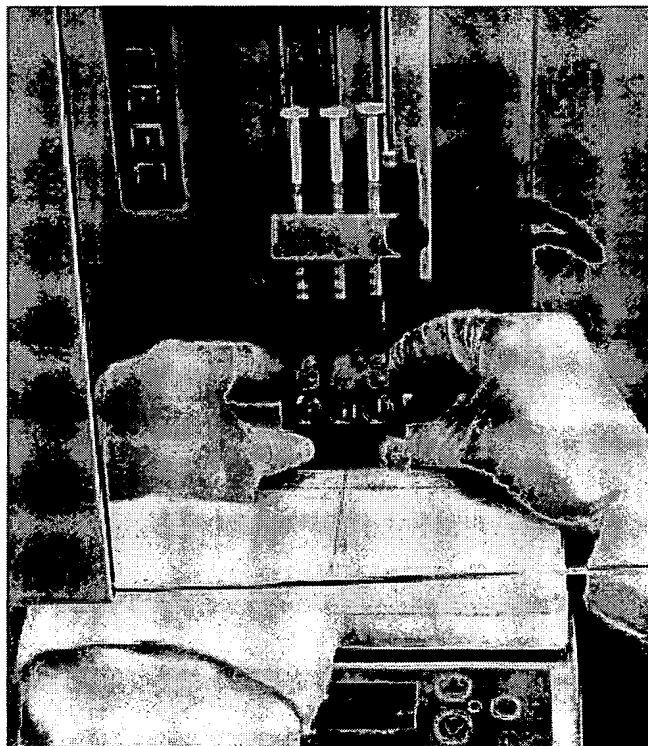


FIG. 32

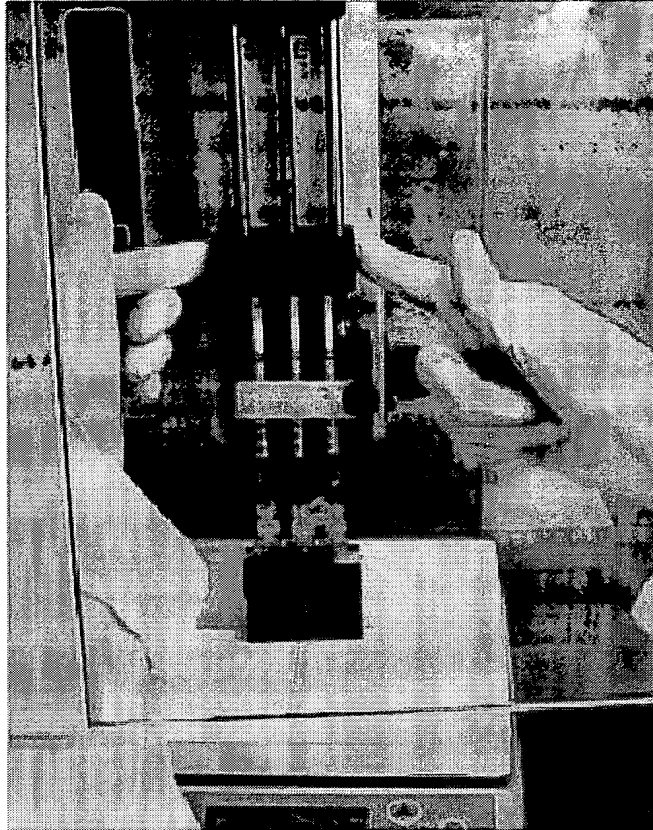


FIG. 33

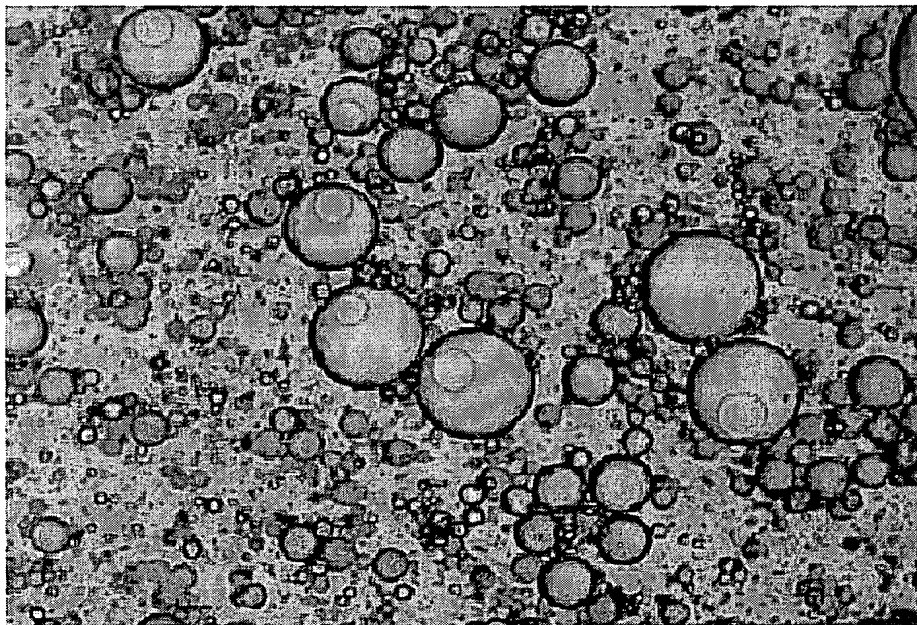
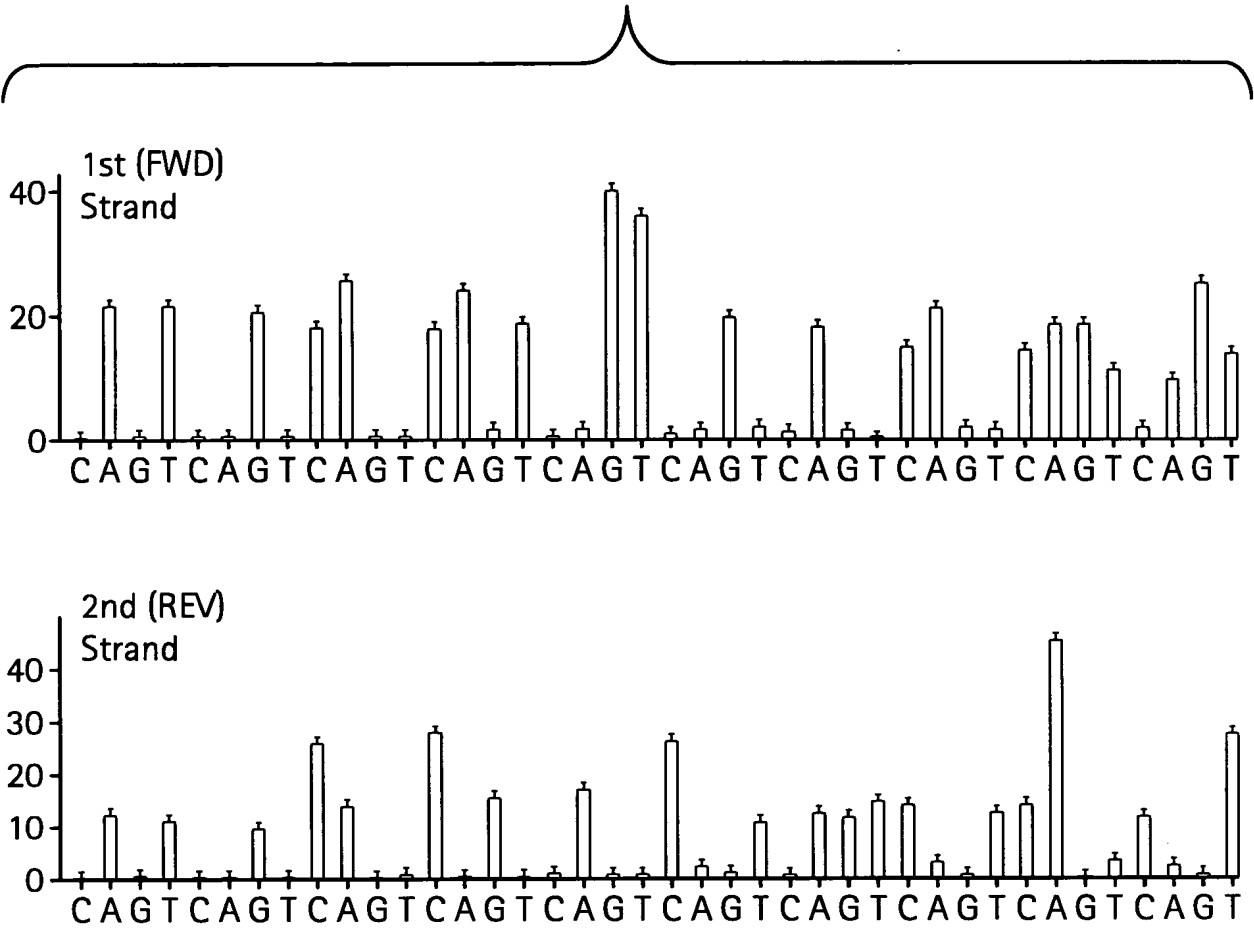


FIG. 34



1st Strand
(FWD)

Sample	Well Location	Sequence	Perfect Match Length
F6_14_1	00001_1362_1660.well	ATGCACATGGTTGACACAGTGGT	22

ATGC ACATGGTTGACACAGTGG

2nd Strand
(REV)

Sample	Well Location	Sequence	Perfect Match Length
F6_14_1	00003_1363_1660.well	ATGCCACCGACCTAGTCTCAAACCT	25

ATGC CACGACCTAGTCTCAAACCT

FIG. 35A



FIG. 35B

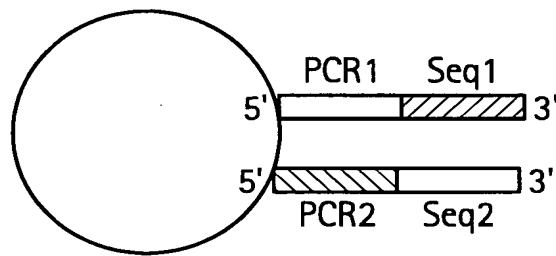


FIG. 35C

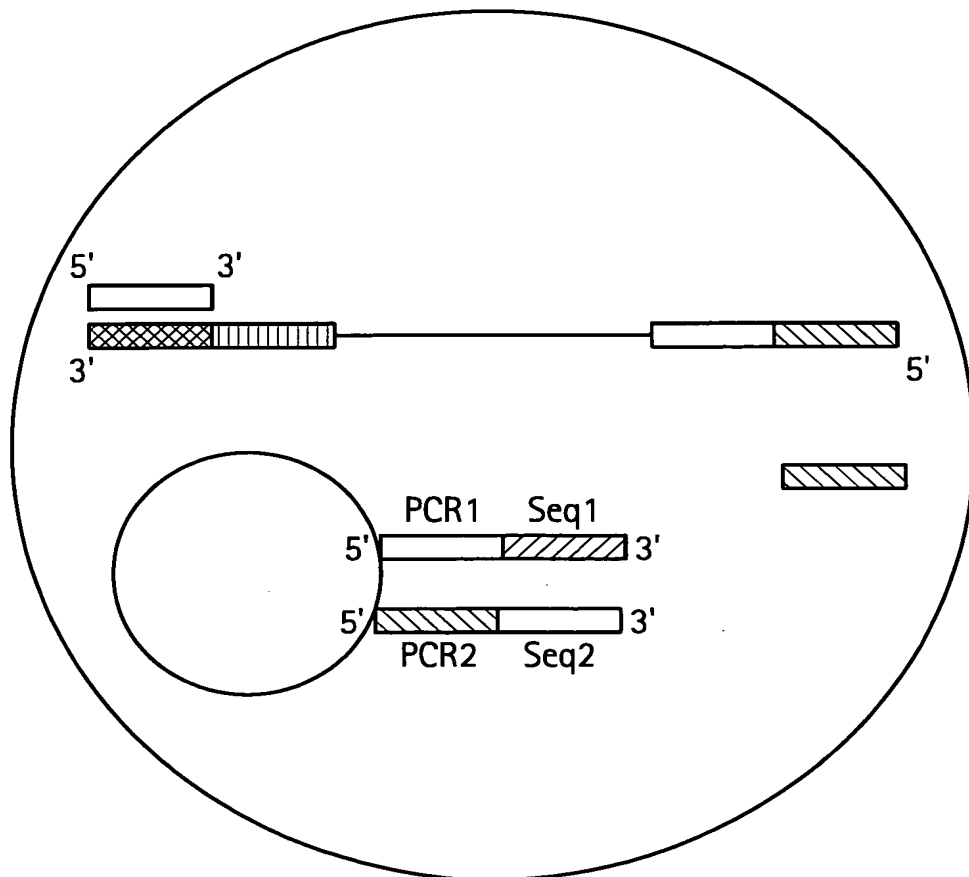


FIG. 36

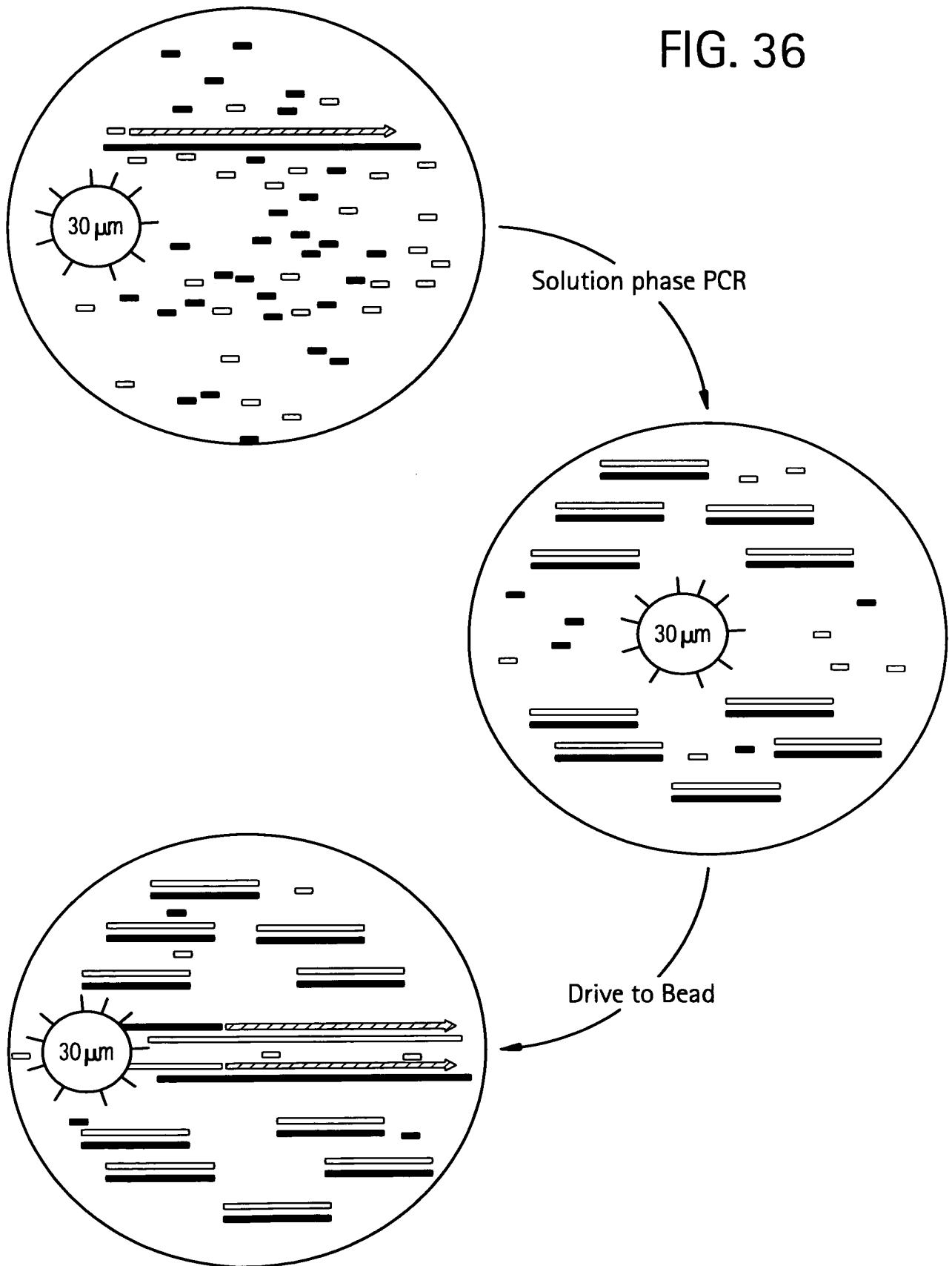
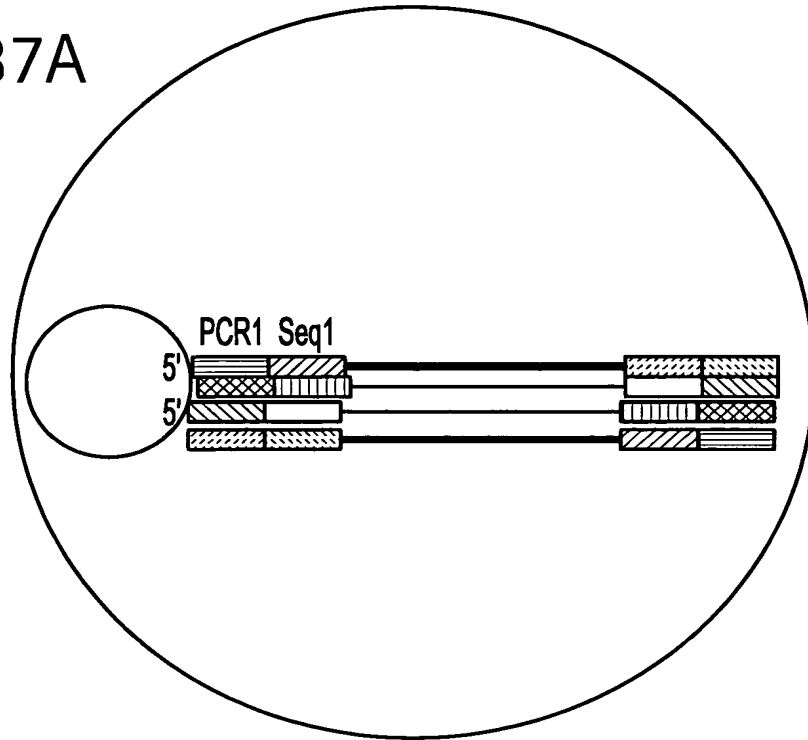


FIG. 37A



Emulsion breaking

FIG. 37B

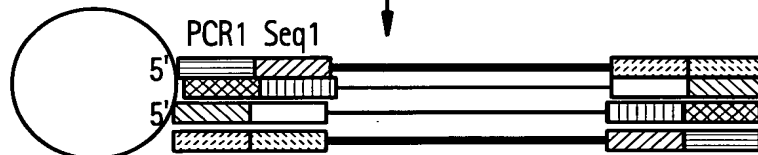
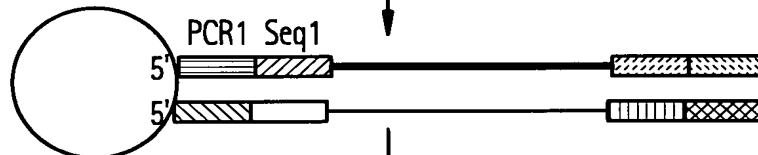
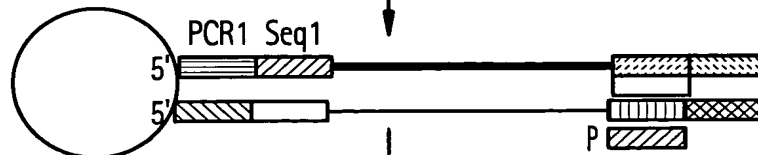
2nd strand removal and
enrichment

FIG. 37C



Annealing sequencing primers

FIG. 37D



1st segment sequencing

FIG. 37E

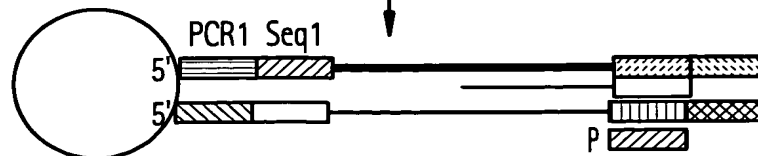


FIG. 38

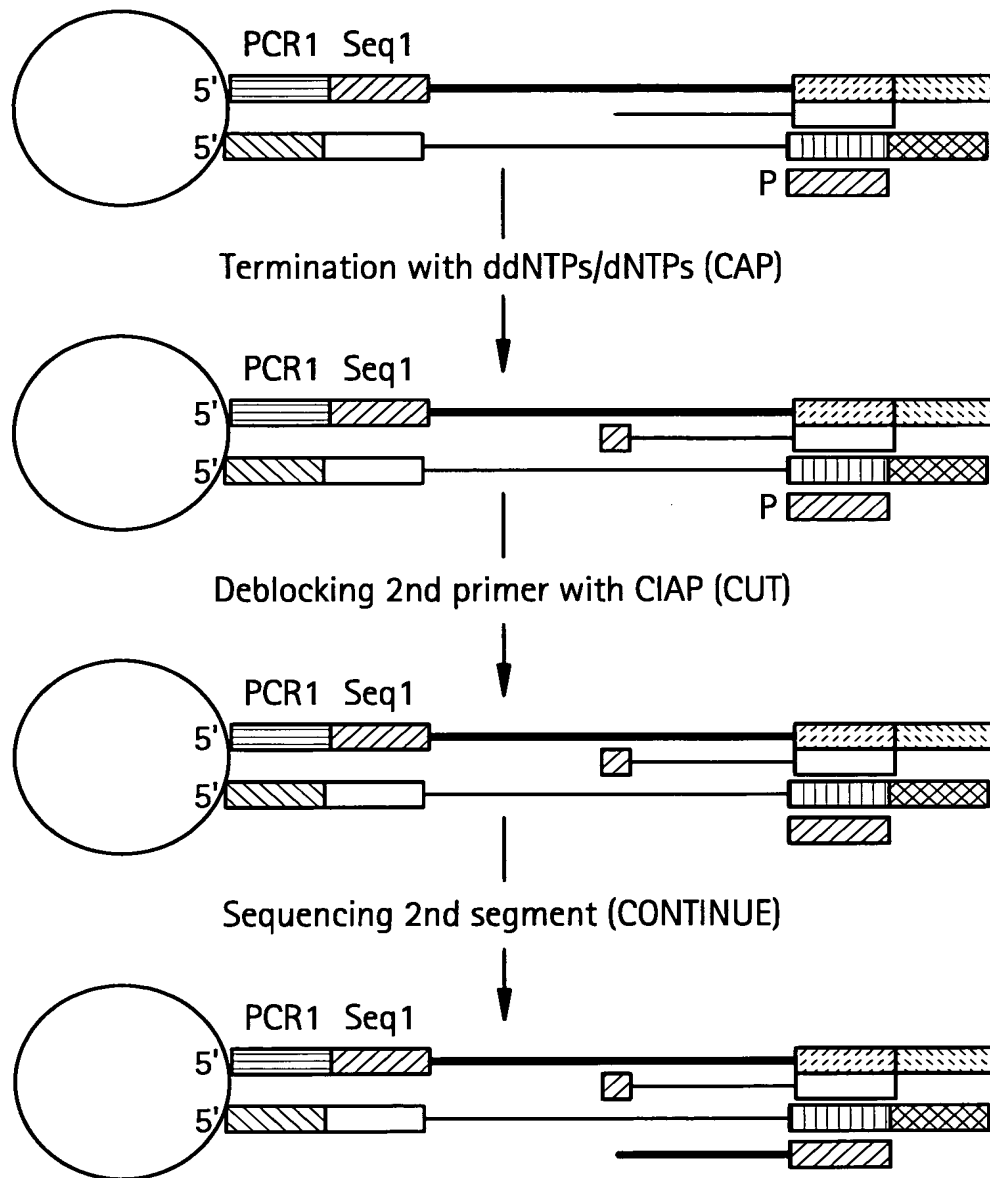


FIG. 39A

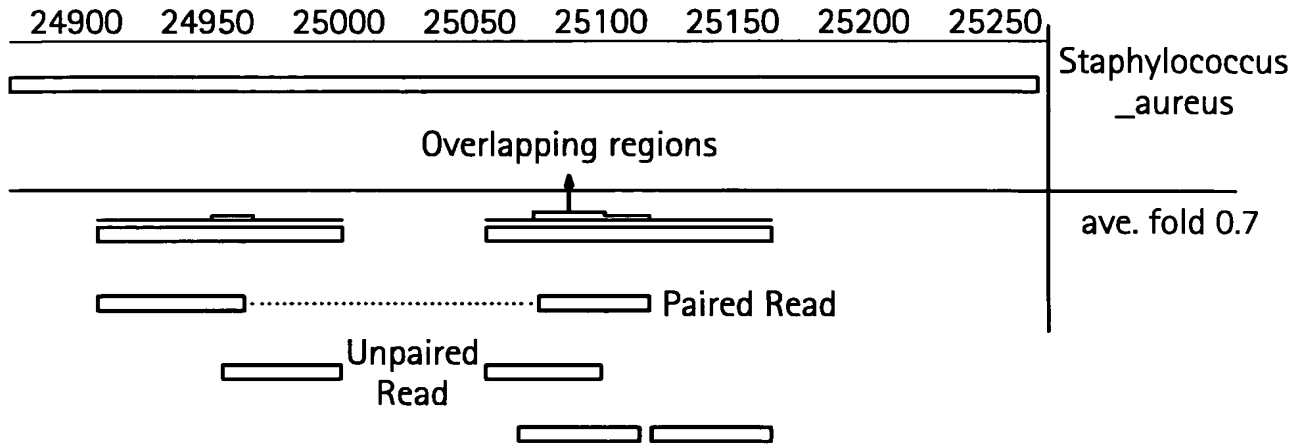


FIG. 39B

Total Reads	31,785
Total 1st Strand	15,770
Total 2nd Strand	16,015
Paired	11,799
Non Paired Reads	8,187
Total Coverage	38%

FIG. 40

Average 95±9 bases

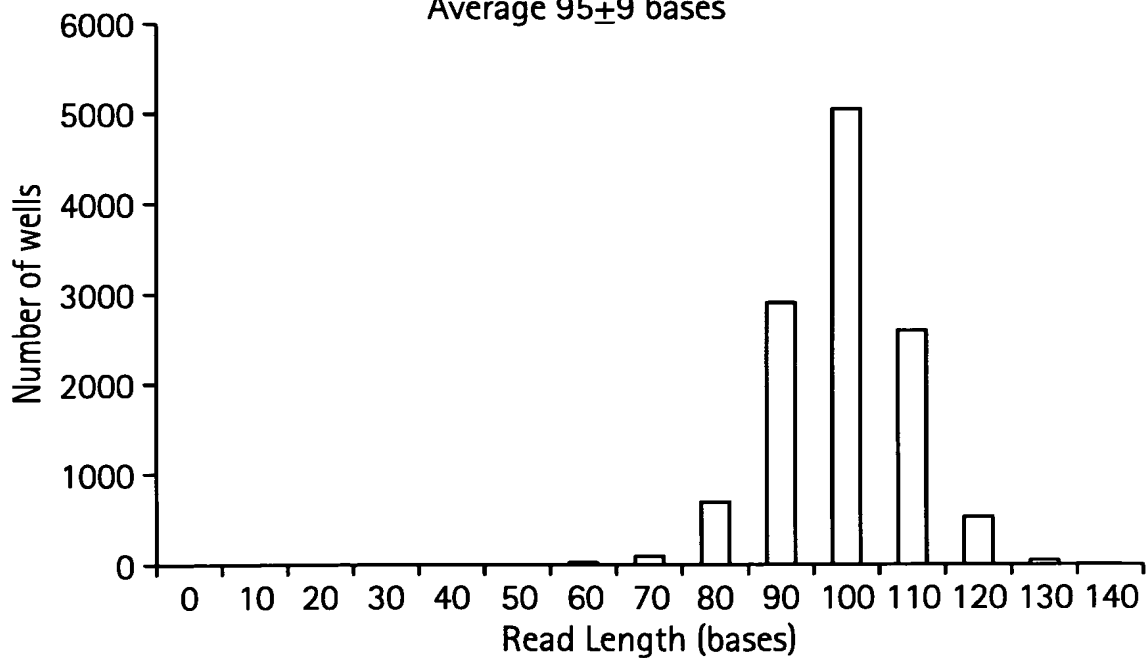


FIG. 41

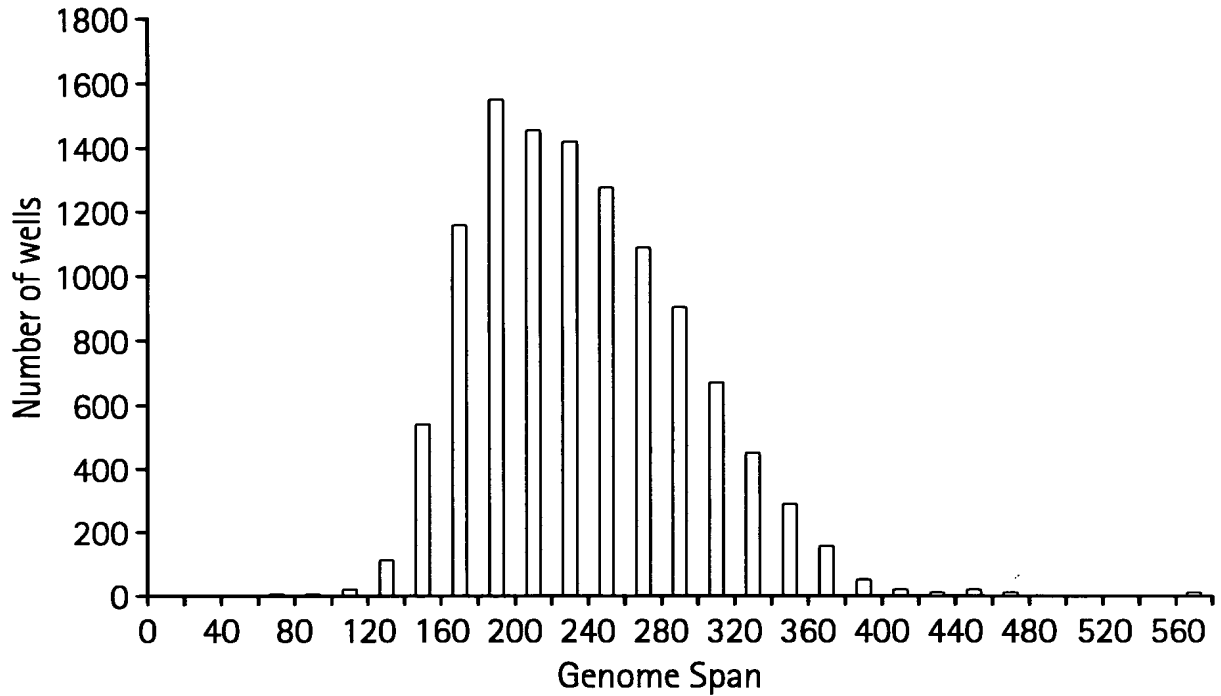


FIG. 42

Well	Genome Position	Orientation	Alignment String
00364_0548_2509	571366	F	TATTGTTGATGCTGTAAAAaGAAGCTACTGGTGTAGtATTTTTATGAAGTT
00364_0548_2509_D2	571512	R	TGCTCAAAGAATTCATTTAAAAATATGACCATATTTCAITGTATCTTT
00383_0985_2232	1487890	R	AAGCGAACAGTCAAGTACCACAGTCAGTTGACtTTTACACAAGCGGAT
00383_0985_2232_D2	1487769	F	TACAGGTGTTGGTATGCCATTGCGATTGTTGCGCTTGGTTAGCCG
00397_0940_2923	2611033	F	AACATATAAACATCCCCTATCTCAATTTCCGCTTCATGTAAaCAAAAAAAGC
00397_0940_2923_D2	2611164	R	TAGATATCACTTGCGTGTTACTGGTAATGCAGGCATGAG
00417_0611_1933	122001	R	ATTCAACTCTGGAAATGCtTTCTTGATACGCCTCGATGATG
00417_0611_1933_D2	121930	F	GATGAGGAGCTGCAATGGCAATGGGTAAAGGCATCATCG
00434_0595_0993	2022591	R	TGTATCTCGATTGGATTAGTTGCTTTTTGCATCTTCATTAGACC
00434_0595_0993_D2	2022473	F	CATTAACATCTGCACCAGAAATAGCTTCTAATACGATTGC
00443_1003_0754	107373	F	GCGACGACGTCCAGCTAATAACGCTGCACCTAAGGCTAATGATAAT
00443_1003_0754_D2	107502	R	AAACCATGCAGATGCTAACAAAGCTCAAGCATTACCAGAACT
00454_1257_3047	59038	R	TGTTGCTGCATCATAATTTAATACTACATCATTTAAAtTCTTTGG
00454_1257_3047_D2	58880	F	GCAGATGGTGTGACTAACCAAGTTGGTCAAAATGCCCTAAATACAAAAGAT